

8-543

198333

mg

From: Jiang, Dong  
Sent: Thursday, August 10, 2006 8:01 PM  
To: STIC-Biotech/ChemLib  
Subject: 10/735,149

Please search SEQ ID NO:28, and 27.

- issued & Pub.
- commercial

Please send results on paper to Dong Jiang in REM 4D70 (mail stop REM 4C70).

Thank you very much.

Dong

Dong Jiang

AU1646  
REM - 4D70  
571-272-0872  
Mail stop REM - 4C70

\*\*\*\*\*  
Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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GenCore version 5.1.9

On nucleic - nucleic search, using sw model  
Run on: August 7, 2006, 12:10:09 : Search time 150 Seconds

Perfect score: 405 (without alignments)  
Sequence: 1 atgcaaggtcaggatcgcca.....acggttccgaaagttcttga 405

Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext: 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Maximum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
listing first 45 summaries

Database : Issued Patents\_NA:  
1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/11\_COMB.seq:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/11\_COMB.seq:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/11\_COMB.seq:\*

9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/11\_COMB.seq:\*

10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	299.6	74.0	483	3	US-09-522-217-63		Sequence 63, Appl
2	299.6	74.0	483	3	US-09-923-246-63		Sequence 63, Appl
3	299.6	74.0	483	3	US-10-295-723-63		Sequence 63, Appl
4	299.6	74.0	623	3	US-09-949-016-436		Sequence 4436, Appl
5	299.6	74.0	642	3	US-09-522-217-1		Sequence 1, Appl
6	299.6	74.0	642	3	US-09-923-246-1		Sequence 1, Appl
7	299.6	74.0	642	3	US-10-295-723-1		Sequence 1, Appl
8	299.6	74.0	642	3	US-10-282-622-1		Sequence 1, Appl
9	296.6	73.2	486	3	US-09-825-561A-9		Sequence 9, Appl
10	294.8	72.8	489	3	US-10-282-622-5		Sequence 5, Appl
11	293.6	72.5	1560	3	US-09-522-217-84		Sequence 84, Appl
12	293.6	72.5	1560	3	US-09-923-246-84		Sequence 84, Appl
13	293.6	72.5	1560	3	US-10-295-723-84		Sequence 84, Appl
14	290.6	71.8	486	3	US-09-522-217-3		Sequence 3, Appl
15	290.6	71.8	486	3	US-09-923-246-3		Sequence 3, Appl
16	290.6	71.8	486	3	US-10-295-723-3		Sequence 3, Appl
17	264.4	65.3	444	3	US-10-282-622-3		Sequence 3, Appl
18	182	44.9	3072	3	US-09-522-217-55		Sequence 55, Appl
19	182	44.9	3072	3	US-09-522-217-55		Sequence 55, Appl
20	182	44.9	3072	3	US-10-295-723-55		Sequence 46, Appl
21	182	44.9	3072	3	US-09-825-561A-16		Sequence 88, Appl
22	175	43.2	1533	3	US-09-522-217-89		Sequence 88, Appl
23	175	43.2	1533	3	US-09-923-246-88		Sequence 88, Appl

24	175	43.2	1533	3	US-10-295-723-88	Sequence 88, Appl
25	105	25.9	12437	3	US-09-949-016-16178	Sequence 16178, A
26	103.4	25.5	103.4	3	US-09-522-217-106	Sequence 106, App
27	103.4	25.5	1656	3	US-09-923-246-106	Sequence 106, App
28	103.4	25.5	1656	3	US-10-295-723-106	Sequence 106, App
29	81.4	20.1	1347	3	US-09-522-217-105	Sequence 105, App
30	81.4	20.1	1347	3	US-10-295-723-105	Sequence 105, App
31	59.6	14.7	535	3	US-09-522-217-4	Sequence 4, Appl
32	59.6	14.7	535	3	US-10-295-723-4	Sequence 4, Appl
33	59.6	14.7	535	3	US-10-295-723-4	Sequence 4, Appl
34	59.6	14.7	535	3	US-10-295-723-4	Sequence 4, Appl
35	58.8	14.5	645	3	US-09-522-217-108	Sequence 108, App
36	58.8	14.5	645	3	US-09-923-246-108	Sequence 108, App
37	58.8	14.5	645	3	US-10-295-723-108	Sequence 108, App
38	44.4	11.0	601	3	US-09-949-016-15862	Sequence 15862, A
39	35.2	8.7	40465	3	US-09-949-016-15261	Sequence 12561, A
40	32	7.9	1600	3	US-09-949-016-1038	Sequence 4038, Ap
41	32	7.9	12113	3	US-09-949-016-1514	Sequence 15144, A
42	32	7.9	13445	3	US-09-949-016-15780	Sequence 15780, A
43	31.6	7.8	73853	3	US-09-949-016-12029	Sequence 12029, A
44	31.4	7.8	1230230	3	US-09-948-185A-1	Sequence 1, Appl
45	31.2	7.7	6819	3	US-09-949-016-12457	Sequence 12457, A

#### ALIGNMENTS

RESULT 1  
US-09-522-217-63

Sequence 63, Application US/09522217  
Patient No. 6307024

GENERAL INFORMATION:  
APPLICANT: NO. 6307024AK, Julia E.

APPLICANT: Presnell, Scott R.

APPLICANT: Sprecher, Cindy A.

APPLICANT: Foster, Donald C.

APPLICANT: Holly, Richard D.

APPLICANT: Gross, Jane A.

APPLICANT: Johnston, Janet V.

APPLICANT: Nelson, Andrew J.

APPLICANT: Dillon, Stacey R.

APPLICANT: Hammond, Angela K.

TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND

FILE REFERENCE: 99-16

CURRENT APPLICATION NUMBER: US/09/522,217

CURRENT FILING DATE: 2000-03-09

EARLIER APPLICATION NUMBER: US 60/123, 547

EARLIER FILING DATE: 1999-03-09

EARLIER FILING DATE: 1999-03-11

EARLIER APPLICATION NUMBER: US 60/142, 013

EARLIER FILING DATE: 1999-07-01

NUMBER OF SEQ ID NOS: 115

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 63

LENGTH: 483

TYPE: DNA

ORGANISM: homo sapiens

US-09-522-217-63

Query Match

74.0%; Score 299.6; DB 3; Length 483;

Best Local Similarity 84.1%; Pred. No. 2.6e-87;

Matches 338; Conservative 0; NisMatches 64; Indels 0; Gaps 0;

Qy

4 CAAGTCAGATGCCACATGATGAGAAGCGCTACTATAGATATGTTGATCAGTCG

63

64 AAAATTATGATGACCTGGTCCGAGATGTTGAGACC 123

33

34

Sequence 3, Appl

Sequence 4, Appl

Sequence 5, Appl

Sequence 6, Appl

Sequence 7, Appl

Sequence 8, Appl

Sequence 9, Appl

Sequence 10, Appl

Sequence 11, Appl

Sequence 12, Appl

Sequence 13, Appl

Sequence 14, Appl

Sequence 15, Appl

Sequence 16, Appl

Sequence 17, Appl

Sequence 18, Appl

Sequence 19, Appl

Sequence 20, Appl

Sequence 21, Appl

Sequence 22, Appl

Sequence 23, Appl

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Sequence 29, Appl

Sequence 30, Appl

Sequence 31, Appl

Sequence 32, Appl

Sequence 33, Appl

Sequence 34, Appl

Sequence 35, Appl

Sequence 36, Appl

Sequence 37, Appl

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Sequence 39, Appl

Sequence 40, Appl

Sequence 41, Appl

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Sequence 43, Appl

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Sequence 45, Appl

Sequence 46, Appl

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Sequence 56, Appl

Sequence 57, Appl

Sequence 58, Appl

Sequence 59, Appl

Sequence 60, Appl

Sequence 61, Appl

Sequence 62, Appl

Sequence 63, Appl

Sequence 64, Appl

Sequence 65, Appl

Sequence 66, Appl

Sequence 67, Appl

Sequence 68, Appl

Sequence 69, Appl

Sequence 70, Appl

Sequence 71, Appl

Sequence 72, Appl

Sequence 73, Appl

Sequence 74, Appl

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Sequence 83, Appl

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Sequence 85, Appl

Sequence 86, Appl

Sequence 87, Appl

Sequence 88, Appl

Sequence 89, Appl

Sequence 90, Appl

Sequence 91, Appl

Sequence 92, Appl

Sequence 93, Appl

Sequence 94, Appl

Sequence 95, Appl

Sequence 96, Appl

Sequence 97, Appl

Sequence 98, Appl

Sequence 99, Appl

Sequence 100, Appl

Sequence 101, Appl

Sequence 102, Appl

Sequence 103, Appl

Sequence 104, Appl

Sequence 105, Appl

Sequence 106, Appl



RESULT 4  
US-09-949-016-4436  
; Sequence 4436, Application US/09949016  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949, 016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241, 755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237, 768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231, 498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 4436  
; LENGTH: 623  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-4436

Query Match 74.0%; Score 299.6; DB 3; Length 623;  
Best Local Similarity 84.1%; Pred. No. 2.9e-87; Indels 0; Gaps 0;  
Matchers 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGCTCAAGTCGCCACATGATTAGATGCTCACTTATAGATTTGTGATCGCTG 63  
Db 134 CAAGGTCAGATGCCACATGATTAGATGCTCACTTATAGATTTGTGATCGCTG 193

Qy 64 AAAATTATGTAAGTCACTGTTGCGGATTCAGAAGGCCGCTCGAGAGGTGAGACC 123  
Db 194 AAAATTATGTAAGTCACTGTTGCGGATTCAGAAGGCCGCTCGAGAGGTGAGACC 253

Qy 124 AACCTGTGAGTGTCTCCCTTCTCCAGAAGGCCGCTCGAGAGGTGAGACC 183  
Db 254 AACCTGTGAGTGTCTCCCTTCTCCAGAAGGCCGCTCGAGAGGTGAGACC 313

Qy 184 GGTAAACACAGAACGATTCATCACGGTTCCATTAAGAACCTGAAACGTAACCGCTCC 183  
Db 254 AACCTGTGAGTGTCTCCCTTCTCCAGAAGGCCGCTCGAGAGGTGAGACC 313

Qy 314 GGAACGATGAGGATAATCATGTCAATTAAAGCTGAAAGGAAACCTCC 373

Db 314 GGAACGATGAGGATAATCATGTCAATTAAAGCTGAAAGGAAACCTCC 373

Qy 244 ACCACGCAAGTGTGTCGAAACCGGTGTGACCTGGCGCTGTGATCTATGAG 303  
Db 374 ACAATGCAAGGAGAACGAGAACGAGAACGACTAACATGCCCTCATGTCTATGAG 433

Qy 304 AAAAACCGCGAAGAACGATCTGGAGGTTCATCCCTCTCGAGAAGATGATTAC 363  
Db 434 AAAAACCGCGAAGAACGATCTGGAGGTTCATCCCTCTCGAGAAGATGATTAC 493

Qy 364 CAGCACCTGTCCTCTGACCGCGTCTCGAGAAGATGATTCTCCAAAGATGATTAC 405  
Db 494 CAGCATCTGTCCTCTGACCGCGTCTCGAGAAGATGATTCTCCAAAGATGATTAC 535

RESULT 5  
US-09-522-217-1  
; Sequence 1, Application US/09522217  
; Patent No. 6307024  
; GENERAL INFORMATION:  
; APPLICANT: Friesen, Scott R.  
; APPLICANT: Gross, Cindy A.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
; APPLICANT: Novel Cytokine Zalpha11 Ligand  
; TITLE OF INVENTION: Novel Cytokine Zalpha11 Ligand  
; FILE REFERENCE: 99-16  
; CURRENT APPLICATION NUMBER: US/09/522, 217  
; CURRENT FILING DATE: 2000-03-09  
; EARLIER APPLICATION NUMBER: US 60/123, 547  
; EARLIER FILING DATE: 1999-03-09  
; EARLIER APPLICATION NUMBER: US 60/123, 904  
; EARLIER FILING DATE: 1999-03-11  
; EARLIER APPLICATION NUMBER: US 60/142, 013  
; EARLIER FILING DATE: 1999-07-01  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO: 1  
; LENGTH: 642  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (47)...(532)  
; US-09-522-217-1

Query Match 74.0%; Score 299.6; DB 3; Length 642;  
Best Local Similarity 84.1%; Pred. No. 2.9e-87; Indels 0; Gaps 0;  
Matchers 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGGTCAGATGCCACATGATTAGATGCTCACTTATAGATTTGTGATCGCTG 63  
Db 134 CAAGGTCAGATGCCACATGATTAGATGCTCACTTATAGATTTGTGATCGCTG 193

Qy 64 AAAATTATGTAAGTCACTGTTGCGGATTCAGAAGGCCGCTCGAGAGGTGAGACC 123  
Db 194 AAAATTATGTAAGTCACTGTTGCGGATTCAGAAGGCCGCTCGAGAGGTGAGACC 253

Qy 124 AACCTGTGAGTGTCTCCCTTCTCCAGAAGGCCGCTCGAGAGGTGAGACC 183  
Db 254 AACCTGTGAGTGTCTCCCTTCTCCAGAAGGCCGCTCGAGAGGTGAGACC 313

Qy 184 GGTAAACACAGAACGATTCATCACGGTTCCATTAAGAACCTGAAACGTAACCGCTCC 183  
Db 254 AACCTGTGAGTGTCTCCCTTCTCCAGAAGGCCGCTCGAGAGGTGAGACC 313

Qy 314 GGAACGATGAGGATAATCATGTCAATTAAAGCTGAAAGGAAACCTCC 373

Db 314 GGAACGATGAGGATAATCATGTCAATTAAAGCTGAAAGGAAACCTCC 373

Qy 244 ACCACGCAAGTGTGTCGAAACCGGTGTGACCTGGCGCTGTGATCTATGAG 303  
Db 374 ACAATGCAAGGAGAACGAGAACGAGAACGACTAACATGCCCTCATGTCTATGAG 433

Qy 304 AAAAACCGCGAAGAACGATCTGGAGGTTCATCCCTCTCGAGAAGATGATTAC 363  
Db 434 AAAAACCGCGAAGAACGATCTGGAGGTTCATCCCTCTCGAGAAGATGATTAC 493

Qy 364 CAGCACCTGTCCTCTGACCGCGTCTCGAGAAGATGATTCTCCAAAGATGATTAC 405  
Db 494 CAGCATCTGTCCTCTGACCGCGTCTCGAGAAGATGATTCTCCAAAGATGATTAC 535

RESULT 6  
US-09-923-246-1  
; Sequence 1, Application US/09923246  
; Patent No. 6605272  
; GENERAL INFORMATION:  
; APPLICANT: No. 6605272ak, Julia E.  
; APPLICANT: Friesen, Scott R.  
; APPLICANT: Spracher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.



```

; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (47)...(532)
; US-10-282-622-1

Query Match 74.0%; Score 299.6; DB 3; Length 642;
Best Local Similarity 84.1%; Pred. No. 2.9e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy 4 CAAGCTCAAGATGCCAACATGATAGAAGCTGCACTATAGATATGTTGATCAGTCG 63
Db 88 CAAGCTCAAGATGCCAACATGATAGAAGCTGCACTATAGATATGTTGATCAGTCG 147
Qy 64 AAAATTATGTAATGCCCTGGTCGGAACTCTGCCCGCTCCGGAAAGCTGAAATCGCAACACC 123
Db 148 AAAATTATGTAATGCCCTGGTCGGAACTCTGCCCGCTCCGGAAAGCTGAAATCGCAACACC 207
Qy 124 AACTCTGAGTGTGTCGCTGTCAGTGTAGAATCGTCAGCTATAGATATGTTGATCAGTCG 183
Db 193 CAAGCTCAAGATGCCAACATGATAGAAGCTGCACTATAGATATGTTGATCAGTCG 193
Qy 64 AAAATTATGTAATGCCCTGGTCGGAACTCTGCCCGCTCCGGAAAGCTGAAATCGCAACACC 123
Db 194 AAAATTATGTAATGCCCTGGTCGGAACTCTGCCCGCTCCGGAAAGCTGAAATCGCAACACC 253
Qy 124 AACTCTGAGTGTGTCGCTGTCAGTGTAGAATCGTCAGCTATAGATATGTTGATCAGTCG 183
Db 254 AACTCTGAGTGTGTCGCTGTCAGTGTAGAATCGTCAGCTATAGATATGTTGATCAGTCG 313
Qy 184 GGTAAACACGTCAGTGTGTCAGTGTAGAATCGTCAGCTATAGATATGTTGATCAGTCG 243
Db 314 GAAACACGTCAGTGTGTCAGTGTAGAATCGTCAGCTATAGATATGTTGATCAGTCG 373
Qy 244 ACCAAACGCAACGTCAGTGTGTCAGTGTAGAATCGTCAGCTATAGATATGTTGATCAGTCG 303
Db 374 ACAAATGCAAGGAGAGACAGAACACAGACTAAATGCTGAAACCGCTGTCAGCTGTCAGTCG 433
Qy 304 AAAAACACGCCGAAGAAATTCTGGAACTGTCATCCATTAAGCTGAAAGGAGATTCCTG 363
Db 434 AAAAACACGCCGAAGAAATTCTGGAACTGTCATCCATTAAGCTGAAAGGAGATTCCTG 493
Qy 364 CAGCACTGTCCTCGTACCCACCGTTCGGAAAGATTCCTG 405
Db 494 CAGCACTGTCCTCGTACCCACCGAAGTTCCTG 535

RESULT 9
US-09-825-561A-9

; Sequence 9, Application US/09825561A
; Patent No. 6,77539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 677539ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: ZALPHALL LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/1337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 5
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: zalphall ligand Q153D/I156D
; NAME/KEY: CDS
; LOCATION: (1)...(489)
; US-10-282-622-5

Query Match 72.8%; Score 294.8; DB 3; Length 489;
Best Local Similarity 83.3%; Pred. No. 9.4e-85;
Matches 335; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
Qy 4 CAAGCTCAAGATGCCAACATGATAGAAGCTGCACTATAGATATGTTGATCAGTCG 63
Db 88 CAAGCTCAAGATGCCAACATGATAGAAGCTGCACTATAGATATGTTGATCAGTCG 147
Qy 64 AAAATTATGTAATGCCCTGGTCGGAACTCTGCCCGCTCCGGAAAGCTGAAATCGCAACACC 123
Db 148 AAAATTATGTAATGCCCTGGTCGGAACTCTGCCCGCTCCGGAAAGCTGAAATCGCAACACC 207
Qy 124 AACTCTGAGTGTGTCGCTGTCAGTGTAGAATCGTCAGCTATAGATATGTTGATCAGTCG 183
Db 208 AACTCTGAGTGTGTCGCTGTCAGTGTAGAATCGTCAGCTATAGATATGTTGATCAGTCG 267
Qy 184 GGTAAACACGTCAGTGTGTCAGTGTAGAATCGTCAGCTATAGATATGTTGATCAGTCG 243
Db 328 ACAAATGCAAGGAGATATCACTAATGCTGAAACAGACTACATGCCCTCATGTCGTTATGAG 387
Qy 304 AAAAACACGCCGAAGAAATTCTGGAACTGTCATCCATTAAGCTGAAAGGAGATTCCTG 363
Db 388 AAAAACACGCCGAAGAAATTCTGGAAAGTTCCTGAAATCATCTCTCCAAAGATGATTCA 447
Qy 364 CAGCACCTGTCCTCGTACCCACGGTTCGGAAAGATTCCTG 402
Db 448 CAGCATCTGTCCTCGTACCCACGGTTCGGAAAGATTCCTG 486

RESULT 10
US-10-282-622-5

; Sequence 5, Application US/10282622
; Patent No. 6929932
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: West, James W.
; APPLICANT: No. 6929932ak, Julia E.
; TITLE OF INVENTION: ZALPHALL LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37
; CURRENT APPLICATION NUMBER: US/10/282,622
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/1337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 5
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: zalphall ligand Q153D/I156D
; NAME/KEY: CDS
; LOCATION: (1)...(489)
; US-10-282-622-5

Query Match 72.8%; Score 294.8; DB 3; Length 489;
Best Local Similarity 83.3%; Pred. No. 9.4e-85;
Matches 335; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
Qy 4 CAAGCTCAAGATGCCAACATGATAGAAGCTGCACTATAGATATGTTGATCAGTCG 63
Db 88 CAAGCTCAAGATGCCAACATGATAGAAGCTGCACTATAGATATGTTGATCAGTCG 147
Qy 64 AAAATTATGTAATGCCCTGGTCGGAACTCTGCCCGCTCCGGAAAGCTGAAATCGCAACACC 123
Db 148 AAAATTATGTAATGCCCTGGTCGGAACTCTGCCCGCTCCGGAAAGCTGAAATCGCAACACC 207
Qy 124 AACTCTGAGTGTGTCGCTGTCAGTGTAGAATCGTCAGCTATAGATATGTTGATCAGTCG 183
Db 208 AACTCTGAGTGTGTCGCTGTCAGTGTAGAATCGTCAGCTATAGATATGTTGATCAGTCG 267

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RESULT 11  
US-09-522-217-84  
; Sequence 84, Application US/09522217  
; Patent No. 6307024  
; GENERAL INFORMATION:  
; APPLICANT: NO. 6307024ak, Julia E.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAI1 LIGAND  
FILE REFERENCE: 99-16  
CURRENT APPLICATION NUMBER: US/09/522-217  
CURRENT FILING DATE: 2000-03-09  
; EARLIER APPLICATION NUMBER: US 60/123,547  
; EARLIER FILING DATE: 1999-03-09  
; EARLIER APPLICATION NUMBER: US 60/123,904  
; EARLIER FILING DATE: 1999-03-11  
; EARLIER APPLICATION NUMBER: US 60/142,013  
; EARLIER FILING DATE: 1999-07-01  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: Fast-SEQ for Windows Version 3.0  
; LENGTH: 1560  
; SEQ ID NO: 84  
; LENGTH: 1560  
; TYPE: DNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1560)  
; OTHER INFORMATION: MBP-human zalphai1 Ligand fusion polynucleotide  
; US-09-522-217-84  
Query Match 72.5%; Score 293.6; DB 3; Length 1560;  
Best Local Similarity 83.8%; Pred. No. 4.1e-85;  
Matches 332; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 10 CAAGATCCACATGATGAGATGCGTCRACTATAGATATGTTGATCAGCTGAAAT 69  
Db 1165 CAAGATCCACATGATGAGATGCGTCRACTATAGATATGTTGATCAGCTGAAAT 1224  
QY 70 TATGTGATGACTGGTTCGGAATTCTCCGCGCTCCGAGATGTTGAGACACTGT 129  
Db 1225 TATGTGATGACTGGTTCGGAATTCTCCGCGCTCCGAGATGTTGAGACACTGT 1284  
Db 1285 GAGTGGTTCGCTTCTCTGTTGAGGCCAACTTAAGTCAGCAATCGAAC 1344  
QY 130 GAGTGGTTCGCTTCTCTGTTGAGGCCAACTTAAGTCAGCAATCGAAC 189  
Db 1285 GAGTGGTTCGCTTCTCTGTTGAGGCCAACTTAAGTCAGCAATCGAAC 1344  
QY 190 AACGAACTTATCATCAACGTTCCATTAAACTGAAACGTTAACCGCGTAC 249  
Db 1345 AACGAACTTATCATCAACGTTCCATTAAACTGAAACGTTAACCGCGTAC 1404  
Db 1525 CTGTCCTCTAGAACACAGGAAGTGAAGATTCTGA 1560

RESULT 12  
US-09-923-246-84  
; Sequence 84, Application US/09923246  
; Patent No. 6605272  
; GENERAL INFORMATION:  
; APPLICANT: NO. 6605272ak, Julia E.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAI1 LIGAND  
FILE REFERENCE: 99-16  
CURRENT APPLICATION NUMBER: US/09/923-246  
CURRENT FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522-217  
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01  
; NUMBER OF SEQ ID NOS: 115  
; SOFTWARE: Fast-SEQ for Windows Version 3.0  
; LENGTH: 1560  
; SEQ ID NO: 84  
; LENGTH: 1560  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1560)  
; OTHER INFORMATION: MBP-human zalphai1 Ligand fusion polynucleotide  
; US-09-923-246-84  
Query Match 72.5%; Score 293.6; DB 3; Length 1560;  
Best Local Similarity 83.8%; Pred. No. 4.1e-85;  
Matches 332; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 10 CAAGATCCACATGATGAGATGCGTCRACTATAGATATGTTGATCAGCTGAAAT 69  
Db 1165 CAAGATCCACATGATGAGATGCGTCRACTATAGATATGTTGATCAGCTGAAAT 1224  
QY 70 TATGTGATGACTGGTTCGGAATTCTCCGCGCTCCGAGATGTTGAGACACTGT 129  
Db 1225 TATGTGATGACTGGTTCGGAATTCTCCGCGCTCCGAGATGTTGAGACACTGT 1284  
QY 130 GAGTGGTTCGCTTCTCTGTTGAGGCCAACTTAAGTCAGCAATCGAAC 189  
Db 1285 GAGTGGTTCGCTTCTCTGTTGAGGCCAACTTAAGTCAGCAATCGAAC 1344  
QY 190 AACGAACTTATCATCAACGTTCCATTAAACTGAAACGTTAACCGCGTAC 249  
Db 1345 AACGAACTTATCATCAACGTTCCATTAAACTGAAACGTTAACCGCGTAC 1404  
Db 1525 CTGTCCTCTAGAACACAGGAAGTGAAGATTCTGA 1560



RESULT 15  
 US-09-923-246-3  
 ; Sequence 3, Application US/09923246  
 ; Pattern No. 6605272  
 ; GENERAL INFORMATION:  
 ; APPLICANT: No. 6605272  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: Sprecher, Cindy A.  
 ; APPLICANT: Foster, Donald C.  
 ; APPLICANT: Holly, Richard D.  
 ; APPLICANT: Gross, Jane A.  
 ; APPLICANT: Johnston, Janet V.  
 ; APPLICANT: Nelson, Andrew J.  
 ; APPLICANT: Dillon, Stacey R.  
 ; APPLICANT: Hammond, Angela K.  
 ; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND  
 ; FILE REFERENCE: 99-16  
 ; CURRENT APPLICATION NUMBER: US/09/923, 246  
 ; CURRENT FILING DATE: 2001-08-03  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522, 217  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123, 904  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142, 013  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01  
 ; NUMBER OF SEQ ID NOS: 115  
 ; SOFTWARE: Fast-SEQ for Windows Version 3.0  
 ; SEQ ID NO: 3  
 ; LENGTH: 486  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Degenerate polynucleotide sequence for human  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(486)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-923-246-3

Query Match  
 Best Local Similarity 71.8%; Score 290.6; DB 3; Length 486;  
 Matches 225; Conservative 114; Mismatches 59; Indels 0; Gaps 0;  
 Qy 4 CAAAGTCAGATCCTCACATGATAGAATGGTCAACTATAGATATGTTGATCAGCTG 63  
 Db 88 CARGGCAGGAGCAGTATGNGATAGTNGNATAGMNCARYNTATHGAVATGCTNGCARYTN 147  
 Qy 64 AAAATTATGTAATGACCTGTCGGAAATTCTCGCCGGCTCCGGAAAGATGTTGAGACC 123  
 Db 148 ARAAYATGATGTTAAGYGAATTGTTGTCAGTAAACGTTCAATGAAACGTTAACGGCCGRC 207  
 Qy 124 ACTGTGACTGTGTCGCTTCTCCGTGTTCCAGAAAGGCCAGCTGAAATCCGCAACACC 183  
 Db 208 AATGGTGTGWSNGCNNTTWSNTGTTGTTGATGTCGACCTGCCGCTCTGTGATCTTATGAG 267  
 Qy 184 GGTAAACGAGGAACTATCCTAACGTTCAATGAAACGTTAACGGCCGRC 243  
 Db 268 GGNAAAYAAYGARMNATHAATTAAYGTWNNSNATHAARAACTGNTAARMGNARCCCNCSN 327  
 Qy 244 ACCAACGAGGTCGTCGTCAGAACACCTGTCGACTGCCGCTCTGTGATCTTATGAG 303  
 Db 328 ACNAAYGCNGNMGNGNCARARCAVMNTYNACTGVCNNWSNTGCAWSNTAYGAR 387

Qy 304 AAAAACCCGAAAGAATTCTCGAAGCTTCATCCCTGCTGAGAAATGATTAC 363  
 Db 388 AARARCCNCNCAARGARTTYTNGARMNTTAAWSNTYNTNCARARATGATHCAY 447  
 Qy 364 CAGCACCTCTCTGACCCAGGTTCGGAAAGATTC 401  
 Db 448 CARCAYYTWNWSNMGNAACNCAYGNNWSNGARGAYWS 485

Search completed: August 7, 2006, 12:12:48  
 Job time : 151 secs





RESULT 4  
US-10-787-442-63  
Sequence 63, Application US/10787442  
; Publication No. US20040260065A1  
; GENERAL INFORMATION:  
; APPLICANT: Novak, Julia B.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnson, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND  
CURRENT APPLICATION NUMBER: US/10/787,442  
CURRENT FILING DATE: 2004-02-26  
PRIOR APPLICATION NUMBER: US/09/522,217  
PRIOR FILING DATE: 2000-03-09  
PRIOR APPLICATION NUMBER: US 60/123,547  
PRIOR FILING DATE: 1999-03-09  
PRIOR APPLICATION NUMBER: US 60/123,904  
PRIOR FILING DATE: 1999-03-11  
PRIOR APPLICATION NUMBER: US 60/142,013  
PRIOR FILING DATE: 1999-07-01  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 63  
LENGTH: 483  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-787-442-63

Query Match 74.0%; Score 299, 6; DB 9; Length 483;  
Best Local Similarity 84.1%; Pred. No. 1.5e-87;  
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGGTCAAGTGCCACATGTTAGATGGTCAACTTATAGATATTGTGATCAGCTG 63  
Db 82 CAAGGTCAAGTGCCACATGTTAGATGGTCAACTTATAGATATTGTGATCAGCTG 141  
Qy 54 AAAATATGGTGAATGCCGTTCTCTGTCCGAATTCGGAACTCCGGCTCCGGAGATGGTGGAC 123  
Db 142 AAAATATGGTGAATGCCGTTCTCTGTCCGAATTCGGAACTCCGGCTCCGGAGATGGTGGAC 201  
Qy 124 ACTGTGAGTGGTCCGTTCTCTGTCCGAATTCGGAACTCCGGCTCCGGAGATGGTGGAC 183  
Db 202 ACTGTGAGTGGTCCGTTCTCTGTCCGAATTCGGAACTCCGGCTCCGGAGATGGTGGAC 261  
Qy 124 ACTGTGAGTGGTCCGTTCTCTGTCCGAATTCGGAACTCCGGCTCCGGAGATGGTGGAC 183  
Db 184 GTTAACACAGCAAGCTATCATACGTTCTAAAAACTGAACTGAAACCGCGCTC 243  
Db 262 GGAACGATGAAAGGATAATCATATGATCAATTAAAGCTGAGGAGAACCTTC 321  
Qy 244 ACCAACCGGAGGTGTCGTCGAAGAACACCGGTCTGACCTGGCCCTCTGTGATCTTAGAG 303  
Db 322 ACAATGCGAGGAAAGTTCAGTCAATTAAAGCTGAAACAGAGCTAACATGCTCTGTGATCTTAGAG 381  
Qy 304 AAAAACGCCAGAAGTTCAGTCTGGAGCTTCAGTCAATTCCCTCTGTGAGAAATGATTCAC 363  
Db 382 AAAAACCCAGAAGTTCAGTCAATTCCCTCTGTGAGAAATGATTCAC 441  
Db 442 CAGCAGTGTCTCTGAGAACACAGGAGTGAAGATTCCTGA 483

RESULT 5  
US-10-775-204-2157  
; Sequence 2157, Application US/10775204  
; Publication No. US20050186664A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A. William A.  
; APPLICANT: Haseltine, William A.  
; APPLICANT: Balance, David J.  
; APPLICANT: Turner, Andrew J.  
TITLE OR INVENTION: Albumin Fusion Proteins  
FILE REFERENCE: PFS64  
CURRENT APPLICATION NUMBER: US/10/775, 204  
CURRENT FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/341, 811  
PRIOR FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/360, 000  
PRIOR FILING DATE: 2002-02-28  
PRIOR APPLICATION NUMBER: 60/378, 950  
PRIOR FILING DATE: 2002-05-10  
PRIOR APPLICATION NUMBER: 60/398, 008  
PRIOR FILING DATE: 2002-07-24  
PRIOR APPLICATION NUMBER: 60/411, 355  
PRIOR FILING DATE: 2002-09-18  
PRIOR APPLICATION NUMBER: 60/414, 984  
PRIOR FILING DATE: 2002-10-02  
PRIOR APPLICATION NUMBER: 60/417, 611  
PRIOR FILING DATE: 2002-10-11  
PRIOR APPLICATION NUMBER: 60/420, 246  
PRIOR FILING DATE: 2002-10-23  
PRIOR APPLICATION NUMBER: 60/423, 623  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/351, 360  
PRIOR FILING DATE: 2002-01-28  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2222  
SOFTWARE: PatentIn ver. 2.0  
SEQ ID NO 2157  
LENGTH: 489  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-775-204-2157

Query Match 74.0%; Score 299, 6; DB 10; Length 489;  
Best Local Similarity 84.1%; Pred. No. 1.5e-87;  
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGGTCAAGTGCCACATGTTAGATGGTCAACTTATAGATATTGTGATCAGCTG 63  
Db 88 CAAGGTCAAGTGCCACATGTTAGATGGTCAACTTATAGATATTGTGATCAGCTG 147  
Qy 64 AAAATATGGTGAATGCCGTTCTCTGTCCGAATTCGGAACTCCGGCTCCGGAGATGGTGGAC 123  
Db 148 AAAATATGGTGAATGCCGTTCTCTGTCCGAATTCGGAACTCCGGCTCCGGAGATGGTGGAC 207  
Qy 124 ACTGTGAGTGGTCCGTTCTCTGTCCGAATTCGGAACTCCGGCTCCGGAGATGGTGGAC 183  
Db 208 AACTGTGAGTGGTCCGTTCTCTGTCCGAATTCGGAACTCCGGCTCCGGAGATGGTGGAC 267  
Qy 184 GTTAACACAGCAAGCTATCATACGTTCTAAAAACTGAACTGAAACCGCGCTC 243  
Db 268 GGAACGATGAAAGGATAATCATATGATCAATTAAAGCTGAGGAGAACCTTC 327

RESULT 6  
US-09-923-246-1  
; Sequence 1, Application US/09923246  
; Patent No. US2002018446A1  
; GENERAL INFORMATION:  
; APPLICANT: NO. US2002018446A1  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND  
FILE REFERENCE: 99-16  
CURRENT APPLICATION NUMBER: US/09/923, 246  
CURRENT FILING DATE: 2001-08-03  
PRIORITY APPLICATION NUMBER: EARLIER FILING DATE: 2000-03-09  
PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123, 904  
PRIORITY FILING DATE: EARLIER FILING DATE: 1999-03-11  
PRIORITY APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142, 013  
PRIORITY FILING DATE: EARLIER FILING DATE: 1999-07-01  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 642  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE: CDS  
NAME/KEY: CDS  
LOCATION: (47) . . . (532)  
US-10-293-246-1  
Query Match 74.0%; Score 299.6; DB 3; Length 642;  
Best Local Similarity 84.1%; Pred. No. 1.7e-87;  
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 4 CAAGGTCAAGATGCCACATGATAGAATGCCAACTTATAGATATTGTCAGCTG 63  
Db 134 CAAGGTCAAGATGCCACATGATAGAATGCCAACTTATAGATATTGTCAGCTG 193  
QY 64 AAAATTATGTAATGACTGTTCTGTTCTAGAGGCCAACTAAAGTCA 123  
Db 194 AAAATTATGTAATGACTGTTCTGTTCTAGAGGCCAACTAAAGTCA 253  
Db 194 AAAATTATGTAATGACTGTTCTGTTCTAGAGGCCAACTAAAGTCA 253  
QY 124 AACTGTGACTGGTCGCTTCTCGTCCAGAAACCCGCTGAATCCGAAACCC 183  
Db 254 AACTGTGACTGGTCGCTTCTCGTCCAGAAACCCGCTGAATCCGAAACCC 313  
Db 254 AACTGTGACTGGTCGCTTCTCGTCCAGAAACCCGCTGAATCCGAAACCC 313  
QY 184 GGTAACAACTAAAGTCACTTAAAGTCAACTTAAAGTCAACTTAAAGTCA 243  
Db 314 GGAAACAACTAAAGTCACTTAAAGTCAACTTAAAGTCAACTTAAAGTCA 373  
Db 314 GGAAACAACTAAAGTCACTTAAAGTCAACTTAAAGTCAACTTAAAGTCA 373  
QY 244 ACCACACGGGTCCTCGTCCAGAAACCCGCTGAATCCGAAACCCGCTGAATCCGAAACCC 303  
QY 374 ACAATGAGGGAGAGAGACAAACAGACTACATGCCCTCATGATCTTATGAG 433  
Db 304 AAAAACCGGAAAGATTCCTGGAGAGTTCAAACCTGCTGAGAAAGTAC 363  
Db 434 AAAAACCGGAAAGATTCCTGGAGAGTTCAAACCTGCTGAGAAAGTAC 493  
QY 364 CAGGACCTCTCTGTAACCCAGGGTCGGAGATTCCTGA 405  
Db 494 CAGGACCTCTCTGTAACCCAGGGTCGGAGATTCCTGA 535  
QY 448 CAGGATCTCTCTGTAACACAGGAAGTCACTCTCCAAAGATGATTCAT 447  
QY 405 CAGGATCTCTCTGTAACACAGGAAGTCACTCTCCAAAGATGATTCAT 489  
RESULT 7  
US-10-295-723-1  
; Sequence 1, Application US/10295723  
; Publication No. US20030125524A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20030125524A1  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Hammond, Angela K.  
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND  
FILE REFERENCE: 99-16  
CURRENT APPLICATION NUMBER: US/10/295, 723  
CURRENT FILING DATE: 2002-11-15  
PRIORITY APPLICATION NUMBER: 09/522, 217  
PRIORITY FILING DATE: 2000-03-09  
PRIORITY APPLICATION NUMBER: US 60/123, 547  
PRIORITY FILING DATE: 1999-03-09  
PRIORITY APPLICATION NUMBER: US 60/123, 904  
PRIORITY FILING DATE: 1999-03-11  
PRIORITY APPLICATION NUMBER: US 60/142, 013  
PRIORITY FILING DATE: 1999-07-01  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 642  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE: CDS  
NAME/KEY: CDS  
LOCATION: (47) . . . (532)  
US-10-295-723-1  
Query Match 74.0%; Score 299.6; DB 7; Length 642;  
Best Local Similarity 84.1%; Pred. No. 1.7e-87;  
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
QY 4 CAAGGTCAAGATGCCACATGATAGAATGCCAACTTATAGATATTGTCAGCTG 63  
Db 134 CAAGGTCAAGATGCCACATGATAGAATGCCAACTTATAGATATTGTCAGCTG 193  
QY 64 AAAATTATGTAATGACTGTTCTGTTCTAGAGGCCAACTAAAGTCA 123  
Db 194 AAAATTATGTAATGACTGTTCTGTTCTAGAGGCCAACTAAAGTCA 253  
QY 124 AACTGTGACTGGTCGCTTCTCGTCCAGAAACCCGCTGAATCCGAAACCC 183  
Db 254 AACTGTGACTGGTCGCTTCTCGTCCAGAAACCCGCTGAATCCGAAACCC 313  
QY 184 GGTAACAACTAAAGTCACTTAAAGTCAACTTAAAGTCAACTTAAAGTCA 243  
Db 314 GGAAACAACTAAAGTCACTTAAAGTCAACTTAAAGTCAACTTAAAGTCA 373  
QY 244 ACCACACGGGTCCTCGTCCAGAAACCCGCTGAATCCGAAACCCGCTGAATCCGAAACCC 303  
QY 374 ACAATGAGGGAGAGAGACAAACAGACTACATGCCCTCATGATCTTATGAG 433  
QY 304 AAAAACCGGAAAGATTCCTGGAGAGTTCAAACCTGCTGAGAAAGTAC 363

RESULT 8  
US-10-282-622-1  
Sequence 1, Application US/10282622  
; Publication No. US0030134390A1  
; GENERAL INFORMATION:  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: West, James W.  
; APPLICANT: No. US2003134390A1ak, Julia E.  
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS  
; CURRENT APPLICATION NUMBER: US/10/282, 622  
; CURRENT FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: 60/337,586  
; PRIOR FILING DATE: 2001-11-05  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 642  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (47) . . . (532)  
US-10-282-622-1

Query Match 74.0%; Score 299.6; DB 7; Length 642;  
Best Local Similarity 84.1%; Pred. No. 1.7e-87;  
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
Query 4 CAAAGTCAGTCGGCACATATTAGATGGTCACTTATAGATATGTCAGCTG 63  
Db 134 CAAAGTCAGATGCCACATGATGTTAGA 193  
Query 64 AAAAATATGGAATGACCTGGTCCGGAAATTCTGCCTCGGGTCCGGAGATGTTGAGCC 123  
Db 194 AAAAATATGGAATGACTGGTCCCTGAATTCTGCCAGTCCAGAAGATGAGAGACA 253  
Query 124 ACTGTGAGTGTCCCTTCTCTCTTCCAGAAGGCCAGCTGAAATCCGAAACACC 183  
Db 254 ACTGTGAGTGTCACTTTCCTGTTCTGAGGCCACTAAAGTCGAATACCTGCAATACA 313  
Query 184 GGTAAACAGCAGCTATCAAGCTTCCATTAAACACTAAACGTAACCGCCAGTGG 243  
Db 314 GGAACAGATGAGGATAATCATGATGATCAATTAAAGCTGAAACCTGCAATACA 373  
Query 244 ACCAACCGAGGTGTCGTCAGAACACCGCTCTGACTGCCGTCGATTCATGAG 303  
Db 374 ACCAACCGAGGTGTCGTCAGAACACCGCTCTGACTGCCGTCGATTCATGAG 433  
Query 304 AAAAACCGGGAAGAATTCTGGACGCTTCATCCCTCTGGAGATTCCTGA 493  
Db 374 AAAAACCGGGAAGAAGACAGAACACAGACTAACATGCTCCCTCATGATCTATGAG 433  
Query 364 CAGCACCTGTCTCTGTACCCACGGTCCGGAAGATTCCTGA 405  
Db 494 CAGCACCTGTCTCTGTACCCACGGTCCGGAAGATTCCTGA 535

RESULT 9  
US-10-456-780-1  
Sequence 1, Application US/10456780  
; Publication No. US2004009150A1  
; GENERAL INFORMATION:  
; APPLICANT: Hughes, Andrew J.  
; APPLICANT: Hughes, Steven D.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Hammond, Angela K.  
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND  
; FILE REFERENCE: 03-08  
; CURRENT APPLICATION NUMBER: US/10/456, 780  
; CURRENT FILING DATE: 2003-06-05  
; PRIOR APPLICATION NUMBER: US 60/387, 127  
; PRIOR FILING DATE: 2002-06-07  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 642  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (47) . . . (532)  
US-10-456-780-1

Query Match 74.0%; Score 299.6; DB 7; Length 642;  
Best Local Similarity 84.1%; Pred. No. 1.7e-87;  
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
Query 4 CAAAGTCAGTCGGCACATATTAGATGGTCACTTATAGATATGTCAGCTG 63  
Db 134 CAAAGTCAGATGCCACATGATGTTAGA 193  
Query 64 AAAAATATGGAATGACCTGGTCCGGAAATTCTGCCTCGGGTCCGGAGATGTTGAGCC 123  
Db 194 AAAAATATGGAATGACTGGTCCCTGAATTCTGCCAGTCCAGAAGATGAGAGACA 253  
Query 124 ACTGTGAGTGTCCCTTCTCTCTTCCAGAAGGCCAGTGGAAATCCGAAACACC 183  
Db 254 ACTGTGAGTGTCACTTTCCTGTTCTGAGGCCACTAAAGTCGAATACCTGCAATACA 313  
Query 184 GGTAAACAGCAGCTATCAAGCTTCCATTAAACACTAAACGTAACCGCCAGTGG 243  
Db 314 GGAACAGATGAGGATAATCATGATGATCAATTAAAGCTGAAACCTGCAATACA 373  
Query 244 ACCAACCGAGGTGTCGTCAGAACACCGCTCTGACTGCCGTCGATTCATGAG 303  
Db 374 AAAAACCGGGAAGAAGACAGAACACAGACTAACATGCTCCCTCATGATCTATGAG 433  
Query 304 AAAAACCGGGAAGAATTCTGGACGCTTCATCCCTCTGGAGATTCCTGA 493  
Db 374 AAAAACCGGGAAGAAGACAGAACACAGACTAACATGCTCCCTCATGATCTATGAG 433  
Query 364 CAGCACCTGTCTCTGTACCCACGGTCCGGAAGATTCCTGA 405  
Db 494 CAGCACCTGTCTCTGTACCCACGGTCCGGAAGATTCCTGA 535

RESULT 10  
US-10-659-684-1  
Sequence 1, Application US/10659684  
; Publication No. US20040110932A1  
; GENERAL INFORMATION:  
; APPLICANT: Novak, Julia E.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Spracher, Cindy A.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Gross, Jane A.  
; APPLICANT: Johnston, Janet V.  
; APPLICANT: Dillon, Stacey R.  
; APPLICANT: Nelson, Andrew J.  
; APPLICANT: Hamm, Angela K.  
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND  
; FILE REFERENCE: 99-16  
; CURRENT APPLICATION NUMBER: US/10/659, 684  
; CURRENT FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: US/09/522, 217  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123, 547

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; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123, 904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142, 013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(532)
; US-10-659-684-1

Query Match 74.0%; Score 299.6; DB 8; Length 642;
Best Local Similarity 84.1%; Pred. No. 1.7e-87;
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Query 4 CAAGGTCAAGATGCCACATGATTAGAATGCGTCAACTTATAGATATGTTTCAGTCG 63
Db 134 CAAGGTCAAGATGCCACATGATTAGAATGCGTCAACTTATAGATATGTTTCAGTCG 193
Query 64 AAAATTATGTTGATGACGTGTTCCGGAATTCGCGGCTCGGAGATGTGAGACC 123
Db 194 AAAATTATGTTGATGACGTGTTCCGGAATTCGCGGCTCGGAGATGTGAGACC 253
Db 124 AACGTGAGTGTGCGCTTCCTCGTTCCGGAAGCGCGATGAAATCCGAAACACC 183
Db 254 AACGTGAGTGTGCGCTTCCTCGTTCCGGAAGCGCGATGAAATCCGAAACACC 313
Query 184 GGTGACAAAGAACCTATCATCAACGGTTTCATTAAGAAACTGAAACGCGGCCGCC 243
Db 314 GGTGACAAAGAACCTATCATCAACGGTTTCATTAAGAAACTGAAACGCGGCCGCC 373
Db 244 ACCACGGAGGTCTCGTCTGAGAACCTGAAACACCGCTGACCTGCCCTGTGATCTT 303
Query 374 ACCACGGAGGTCTCGTCTGAGAACCTGAAACACCGCTGACCTGCCCTGTGATCTT 433
Db 304 AAAAACCGGGAAAGAATTCCTGGAACGTTCAATCCTGCTGAGAAATGATTCAC 363
Query 433 AAAAACCGGGAAAGAATTCCTGGAACGTTCAATCCTGCTGAGAAATGATTCAC 493
Db 364 CAGCACCTGTCCTCGTACCCACGGTTCCAAAGATGATCTG 405
Query 494 CAGCACCTGTCCTCGTACCCACGGTTCCAAAGATGATCTG 535
Db 494 CAGCATCTGTCCTAGAACACAGGAAGTCACTCTG 535

RESULT 11
US-10-787-442-1
; Sequence 1, Application US/10787442
; Publication No. US2004026005A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia B.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew
; APPLICANT: Dillion, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US/09/522,239
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123, 547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123, 904

RESULT 12
US-10-951-239-1
; Sequence 1, Application US/10951239
; Publication No. US20050095223A1
; GENERAL INFORMATION:
; APPLICANT: Sirakumar, Pallavir
; APPLICANT: Nelson, Andrew
; TITLE OF INVENTION: METHODS OF TREATING AUTOIMMUNE DISEASES
; TITLE OF INVENTION: USING IL-21
; FILE REFERENCE: 03-09
; CURRENT APPLICATION NUMBER: US/10/951,239
; CURRENT FILING DATE: 2004-09-27
; PRIOR APPLICATION NUMBER: 60/505,919
; PRIOR FILING DATE: 2003-09-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (47)...(532)
; US-10-951-239-1

Query Match 74.0%; Score 299.6; DB 10; Length 642;

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Best Local Similarity 84.1%; Pred. No. 1.7e-87;  
 Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGGTCAAGTCGCCACATGATTAGATGGTCAACTTATAGATATGTTGATCGCTG 63  
 Db 134 CAAGGTCAAGTCGCCACATGATTAGATGGTCAACTTATAGATATGTTGATCGCTG 193  
 Qy 64 AAAATTATGTAATGACTGTTCCGGAAATTCCTCGCGGTCGGAGATGTTGACGCC 63  
 Db 194 AAAATTATGTAATGACTGTTCCGGAAATTCCTCGCGGTCGGAGATGTTGACGCC 253  
 Qy 124 ACTGTGAGTGGTCCGTTTCCGTGTTCCAGAAGCCAGCTGAAATCCGAACACC 183  
 Db 254 ACTGTGAGTGGTCACTTTCCTGTTCTGAAATTCCTCGCGGTCGGAGATGTTGAC 313  
 Qy 184 CGTAAACACAGCTGTCGAGACAGCTGAAATCCGAACACC 243  
 Db 314 GAAACATGTAATGATGTTGATCGCTGAAATCCGAACACC 373  
 Qy 244 ACCAACCCAGGTGTCGAGACAGCTGAAATCCGAACACC 303  
 Db 374 ACAAATCAGGAGAGACAGACAGACTAACATGCGCTCATGTGATCTATGAG 433  
 Qy 304 AAAAACCGCGGAAGAATCTGGAAAGCTGAAATCCGAACACC 363  
 Db 434 AAAAACCCAGGAAATCTGAAAGATGTCAGTCCAAAGATGATCAT 493  
 Qy 364 CGAACCTGTCCTGTAACCCACGGTCCCGAGATTCCTGA 405  
 Db 494 CAGCATCTGTCCTGAAACACGGAGCTGAGATTCCTGA 535

RESULT 13  
 US-11-174-398-1  
 ; Sequence 1, Application US/11174398  
 ; Publication No. US200502449301  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: West, James W.  
 ; APPLICANT: Novak, Julia E.  
 ; TITLE OF INVENTION: ZALPHA1 LIGAND ANTAGONISTS  
 ; FILE REFERENCE: 01-37  
 ; CURRENT APPLICATION NUMBER: US/11/174,398  
 ; PRIOR APPLICATION NUMBER: US/10/282,622  
 ; PRIOR FILING DATE: 2002-10-28  
 ; PRIOR APPLICATION NUMBER: 60/337,586  
 ; PRIOR FILING DATE: 2001-11-05  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 642  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (47) ... (532)  
 ; US-11-174-398-1

Query Match 74.0%; Score 299,6; DB 15; Length 642;  
 Best Local Similarity 84.1%; Pred. No. 1.7e-87;  
 Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGGTCAAGTCGCCACATGATTAGATGGTCAACTTATAGATATGTTGATCGCTG 63  
 Db 134 CAAGGTCAAGTCGCCACATGATTAGATGGTCAACTTATAGATATGTTGATCGCTG 193  
 Qy 64 AAAATTATGTAATGACTGTTCCGGAAATTCCTCGCGGTCGGAGATGTTGACGCC 63  
 Db 194 AAAATTATGTAATGACTGTTCCGGAAATTCCTCGCGGTCGGAGATGTTGACGCC 253  
 Qy 124 ACTGTGAGTGGTCCGTTTCCGTGTTCCAGAAGCCAGCTGAAATCCGAACACC 183  
 Db 254 ACTGTGAGTGGTCACTTTCCTGTTCCAGAAGCCAGCTGAAATCCGAACACC 313  
 Qy 184 GGTAAACACAGCTGTCGAGACAGCTGAAATCCGAACACC 243  
 Db 314 GAAACATGTAATGATGTTGATCGCTGAAATCCGAACACC 373  
 Qy 244 ACCAACCCAGGTGTCGAGACAGCTGAAATCCGAACACC 303  
 Db 374 ACAAATCAGGAGAGACAGACAGACTAACATGCGCTCATGTGATCTATGAG 433  
 Qy 304 AAAAACCGCGGAAGAATCTGGAAAGCTGAAATCCGAACACC 363

RESULT 15  
 US-11-137-807-11  
 ; Sequence 11, Application US/11137807  
 ; Publication No. US2006034810A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Riley, James  
 ; APPLICANT: June, Carl  
 ; APPLICANT: Vonderheide, Robert  
 ; APPLICANT: Aqui, Nicole  
 ; APPLICANT: Suhoski, Meagan  
 ; TITLE: NOVEL ARTIFICIAL ANTIGEN PRESENTING CELLS AND USES THEREFOR  
 ; FILE REFERENCE: 05893-5054US1  
 ; CURRENT APPLICATION NUMBER: US/11/137,807  
 ; CURRENT FILING DATE: 2005-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/575,712  
 ; PRIOR FILING DATE: 2004-05-27  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 11  
 ; LENGTH: 611  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-11-137-807-11

Query Match      73.6%; Score 298; DB 16; Length 611;  
 Best Local Similarity 83.8%; Pred. No. 5.7e-87; Mismatches 65; Indels 0; Gaps 0;  
 Matches 337; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY      4 CAAGGTCAAGATGCCAGATGATTAGAATGCGTCACTTATAGATATGTTGATCAGTG 63  
 Db      128 CAAGGTCAAGATGCCAGATGATTAGAATGCGTCACTTATAGATATGTTGATCAGTG 187  
 QY      64 AAAATTATGTTGATGACCTGGTCCGGAAATTCTGGCGCGCTCCGGGAGATGTTGAGACC 123  
 Db      188 AAAATTATGTTGATGACCTGGTCCGGAAATTCTGGCGCGCTCCGGGAGATGTTGAGACC 247  
 QY      124 ACTGTGACTGTCGCGCTTCCTGTTCCAGAAAGCCAGCTGAAATCCGAAACCC 183  
 Db      248 ACTGTGACTGTCGCGCTTCCTGTTCCAGAAAGCCAGCTGAAATCCGAAACCC 307  
 QY      184 GTTACACGAACTATCATCAACGTTCCATTAAAACCTGAAACGTTAACGGCCGTTCC 243  
 Db      308 GGAACACATGAAAGATAATCCTAATGTTGATCATTAAAGCTGAAAGGAAACCTTCC 367  
 QY      244 ACCAACCGGGCTCTGTCAGAAACACCTCTGACCTGGCGCTCTGATCTATGAG 303  
 Db      368 ACAATGAGGGAGAGACAGAACACAGACTACATGCGCTCATGTCATGATCTATGAG 427  
 QY      304 AAAAACCGGGAAAGAATTCCTGAAACGTTCAATCCTGCTGAGAAATGATTCAC 363  
 Db      428 AAAAACCGGGAAAGAATTCCTGAAACGTTCAATCCTGCTGAGAAATGATTCAC 487  
 QY      364 CAGCACCTGTCCTGTCAGGTCGGAGATTCCTGAGAAACATCTCCAAAGATCTCA 405  
 Db      488 CAGCATCTGTCCTGAGAAACACGGAGATGAGATTCCTGAG 529

Search completed: August 7, 2006, 12:30:07  
 Job time : 1012 secs

GenCore version 5.1.9									
Copyright (C) 1993 - 2006 Biocceleration Ltd.									
OM nucleic - nucleic search, using sw model									
Run on: August 7, 2006, 12:24:32 ; Search time 1538 Seconds									
417.070 Million cell updates/sec									
Title: US-10-735-149-27	Sequence: 1 argcaagtcaagatcgcca. .... aggttccaaagattctga 405	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	Searched: 2193277 seqs, 791917567 residues	Total number of hits satisfying chosen parameters: 4386554	Minimum DB seq length: 0	Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0%	Maximum Match 100%	LISTING
Database : Published Applications NA New:*	1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/us09_NEW_PUB.seq:*	2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/us07_NEW_PUB.seq:*	3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/us01_NEW_PUB.seq:*	4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/us06_NEw_PUB.seq:*	5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEw_PUB.seq:*	6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/us10_NEw_PUB.seq:*	7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/us11_NEw_PUB.seq:*	8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/us11_NEw_PUB.seq:*	9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/us11_NEw_PUB.seq:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Match Length	DB ID	Description	RESULT 1	US-10-735-149-27	;	Sequence 27, Application US/10735149	ALIGNMENTS
1	405	100	0	405 6 US-10-735-149-27	;	Publication No. US20060134754A1	;	;	
2	299.6	74.0	642	6 US-10-511-937-565	GENERAL INFORMATION:	;	;	;	
3	299.6	74.0	642	6 US-10-735-149-1	APPLICANT: Chan, Chung	;	;	;	
4	299.6	74.0	642	8 US-11-266-748A-401642	APPLICANT: Zamost, Bruce L.	;	;	;	
5	299.6	74.0	642	8 US-11-266-748A-472688	APPLICANT: Covert, Douglas C.	;	;	;	
6	298	73.6	617	6 US-10-806-611-1	APPLICANT: Liu, Hong Y.	;	;	;	
7	182	44.9	3072	6 US-10-806-611-3	APPLICANT: De Jongh, Karen S.	;	;	;	
8	64	15.8	64	6 US-10-735-149-26	APPLICANT: Meyer, Jeffrey D.	;	;	;	
9	63	15.6	63	6 US-10-735-149-25	APPLICANT: Holderman, Susan D.	;	;	;	
10	60	14.8	60	6 US-10-735-149-17	;	;	;	;	
11	60	14.8	60	6 US-10-735-149-18	;	;	;	;	
12	60	14.8	60	6 US-10-735-149-19	;	;	;	;	
13	60	14.8	60	6 US-10-735-149-20	;	;	;	;	
14	60	14.8	60	6 US-10-735-149-21	;	;	;	;	
15	60	14.8	60	6 US-10-735-149-22	;	;	;	;	
16	58.4	14.4	60	6 US-10-735-149-15	;	;	;	;	
17	41	10.1	50	6 US-10-735-149-15	;	;	;	;	
18	40	9.9	40	6 US-10-735-149-11	;	;	;	;	
19	40	9.9	40	6 US-10-735-149-12	;	;	;	;	
20	36.8	9.1	40	6 US-10-735-149-9	;	;	;	;	
21	36.8	9.1	40	6 US-10-735-149-10	;	;	;	;	
22	36	8.9	60	6 US-10-735-149-23	;	;	;	;	
23	32.4	8.0	26087	9 US-11-021-837-19	;	;	;	;	
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RESULT 2  
US-10-511-937-565  
Sequence 565, Application US/10511937  
Publication No. US2006008883A1  
GENERAL INFORMATION:  
APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
APPLICANT: Wong Gemuth, Jay  
APPLICANT: FYV, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
APPLICANT: Prentice, James  
APPLICANT: Morris, MacDonald  
APPLICANT: Rosenberg, Steven  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
FILE REFERENCE: 506612000104  
CURRENT APPLICATION NUMBER: US/10/511, 937  
CURRENT FILING DATE: 2004-10-19  
PRIORITY FILING DATE: 2003-04-24  
PRIORITY APPLICATION NUMBER: PCT/US2003/012946  
SEQ ID NO 565  
LENGTH: 642  
SOFTWARE: PatentIn version 3.2  
ORGANISM: Homo sapiens  
US-10-511-937-565

Query Match 74.0%; Score 299.6; DB 6; Length 642;  
Best Local Similarity 84.1%; Pred. No. 2.6e-91;  
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGGTCAAGATCCACATGATGAGATGCGTCACTTATAGATATTGTGAGCTG 63  
Db 134 CAAGGTCAAGATCCACATGATGAGATGCGTCACTTATAGATATTGTGAGCTG 193  
QY 64 AAAAATTATGTTGATGACTTGCTGCTGATTTGAGATGTTGAGACC 123  
Db 194 AAAAATTATGTTGATGACTTGCTGCTGATTTGAGATGTTGAGACC 253  
QY 124 AACTGTGAGTGGTCGCTTCTCTGTTCCAGAAGGCCAGCTCAAATCCGCAACACC 183  
Db 254 AACTGTGAGTGGTCGCTTCTCTGTTCCAGGCCCCACTTAAGTCAGCAATACA 313  
QY 184 GGTACACAAAGCAACGTTATCATCAACCTTCCATTAAAAGACTGAACAGTAAACCCGTC 243  
Db 194 AAAAATTATGTTGAGATGACTTGCTGCTGATTTGAGATGTTGAGACC 253  
QY 124 AACTGTGAGTGGTCGCTTCTCTGTTCCAGAAGGCCAGCTCAAATCCGCAACACC 183  
Db 254 AACTGTGAGTGGTCGCTTCTCTGTTCCAGGCCCCACTTAAGTCAGCAATACA 313  
QY 184 GGTACACAAAGCAACGTTATCATCAACCTTCCATTAAAAGACTGAACAGTAAACCCGTC 243  
Db 314 GGAACAAATGAAAGGATAATCAATGATCATTAAGCTGAGAAGGAAACACCTCC 373  
QY 244 ACCAAAGCGCGTCGCTGAGAACACCCGCTGAGCTGCCGTCGTCGATCTATAG 303  
Db 374 ACAATGCGGGAGAGCAACAGACTAAATGACGCTTCATGTTGATTCATGAG 433

RESULT 3  
US-10-735-149-1  
Sequence 1, Application US/10735149  
Publication No. US20060134754A1  
GENERAL INFORMATION:  
APPLICANT: Chan, Chung  
APPLICANT: Zamost, Bruce L.  
APPLICANT: Covert, Douglas C.  
APPLICANT: Liu, Hong Y.  
APPLICANT: De Jongh, Karen S.  
APPLICANT: Meyer, Jeffrey D.  
APPLICANT: Holderman, Susan D.  
TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21  
FILE REFERENCE: 02-12  
CURRENT APPLICATION NUMBER: US/10/735,149  
CURRENT FILING DATE: 2003-12-12  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 642  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE: CDS  
NAME/KEY: CDS  
LOCATION: (47) ... (535)  
US-10-735-149-1

Query Match 74.0%; Score 299.6; DB 6; Length 642;  
Best Local Similarity 84.1%; Pred. No. 2.6e-91;  
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGGTCAAGATCCACATGATGAGATGCGTCACTTATAGATATTGTGAGCTG 63  
Db 134 CAAGGTCAAGATCCACATGATGAGATGCGTCACTTATAGATATTGTGAGCTG 193  
QY 64 AAAAATTATGTTGATGACTTGCTGCTGATTTGAGATGTTGAGACC 123  
Db 194 AAAAATTATGTTGATGACTTGCTGCTGATTTGAGATGTTGAGACC 253  
QY 124 AACTGTGAGTGGTCGCTTCTCTGTTCCAGAAGGCCAGCTCAAATCCGCAACACC 183  
Db 254 AACTGTGAGTGGTCGCTTCTCTGTTCCAGGCCCCACTTAAGTCAGCAATACA 313  
QY 184 GGTACACAAAGCAACGTTATCATCAACCTTCCATTAAAAGACTGAACAGTAAACCCGTC 243  
Db 314 GGAACAAATGAAAGGATAATCAATGATCATTAAGCTGAGAAGGAAACACCTCC 373  
QY 244 ACCAAAGCGCGTCGCTGAGAACACCCGCTGAGCTGCCGTCGTCGATCTATAG 303  
Db 374 ACAATGCGGGAGAGCAACAGACTAAATGACGCTTCATGTTGATTCATGAG 433

RESULT 4  
US-11-266-748A-401642

; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnstone, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 48396  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 401642  
; LENGTH: 642  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; US-11-266-748A-401642

Query Match 74.0% Score 299 6; DB 8; Length 642;  
Best Local Similarity 84.1%; Pred. No. 2.6e-91; Mismatches 338; Conservative 0; Indels 0; Gaps 0; Matches 338;

QY 4 CAAGGTCAGTCGCCCCACATGTTAGATGGTCAACTTATAGATATGTTGATCAGTC 63  
Db 134 CAAGGTCAGTCAGTCGCCCCACATGTTAGATGGTCAACTTATAGATATGTTGATCAGTC 193

QY 64 AAAAATTATGTTGAAATGACCTGTTCCGGAATTCCTCGCCGCTCCGGAAAGAGTTGAGACC 123  
Db 194 AAAAATTATGTTGAAATGACCTGTTCCGGAATTCCTCGCCGCTCCGGAAAGAGTTGAGACC 253

QY 124 AACTGTGAGTGTGTCGCTTTCCTCCGTTCCAGAAGAGCCGAGCTGAAATCCGAAACACC 183  
Db 254 AACTGTGAGTGTGTCAGCTTTCCTCCGTTCCAGAAGAGCCGAGCTGAAATCCGAAACACC 313

QY 184 GGTAAACACCGAACGAACTCATCAACGTTCCCTAAAAACTGAAGTAAACCGCGCTC 243  
Db 314 GGTAAACACCGAACGAACTCATCAACGTTCCCTAAAAACTGAAGTAAACCGCGCTC 373

QY 244 ACCAACGCGAGTCGTCGTCAGAACACCGCTTGACTCGCCGCTCGTGATCTATGAG 303  
Db 374 ACACATGCGGGAGAGACAGAACACAGACTAACTGCGCTTCATGTTGATCTATGAG 433

QY 304 AAAAACCGCGGAAGAACTCTGAAAGTTCGAACTGTTCAATCCCTGTCAGAAATGTTAC 363  
Db 434 AAAAACCGCGAACGAACTCTGAAAGTTCGAACTGTTCAATCCCTGTCAGAAATGTTAC 493

QY 364 CAGCACCTGCTCTGTAACACCGTTCCGAGAATTCCTGA 405  
Db 494 CAGCACCTGCTCTGTAACACCGTTCCGAGAATTCCTGA 535

RESULT 5  
US-11-266-748A-472688/C  
; Sequence 472688, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnstone, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; TITLE OF INVENTION: Methods of Using the Same  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 48396  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 472688  
; LENGTH: 642  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; US-11-266-748A-472688

Query Match 74.0% Score 299 6; DB 8; Length 642;  
Best Local Similarity 84.1%; Pred. No. 2.6e-91; Mismatches 338; Conservative 0; Indels 0; Gaps 0; Matches 338;

QY 4 CAAGGTCAGTCGCCCCACATGTTAGATGGTCAACTTATAGATATGTTGATCAGTC 63  
Db 509 CAAGGTCAGTCGCCCCACATGTTAGATGGTCAACTTATAGATATGTTGATCAGTC 450

QY 64 AAAAATTATGTTGAAATGACCTGTTCCGGAATTCCTCGCCGCTCCGGAAAGAGTTGAGACC 123  
Db 449 AAAAATTATGTTGAAATGACCTGTTCCGGAATTCCTCGCCGCTCCGGAAAGAGTTGAGACC 390

QY 124 AACTGTGAGTGTGTCGCTTTCCTCCGTTCCAGAAGAGCCGAGCTGAAATCCGAAACACC 183  
Db 389 AACTGTGAGTGTGTCGCTTTCCTCCGTTCCAGAAGAGCCGAGCTGAAATCCGAAACACC 330

QY 184 GGTAAACACCGAACGAACTCATCAACGTTCCCTAAAAACTGAAGTAAACCGCGCTC 243  
Db 329 GGTAAACACCGAACGAACTCATCAACGTTCCCTAAAAACTGAAGTAAACCGCGCTC 270

QY 244 ACCAACGCGAGTCGTCGTCAGAACACCGCTTGACTCGCCGCTCGTGATCTATGAG 303  
Db 269 ACACATGCGGGAGAGACAGAACACAGACTAACTGCGCTTCATGTTGATCTATGAG 210

QY 304 AAAAACCGCGGAAGAACTCTGAAAGTTCGAACTGTTCAATCCCTGTCAGAAATGTTAC 363  
Db 209 AAAAACCGCGAACGAACTCTGAAAGTTCGAACTGTTCAATCCCTGTCAGAAATGTTAC 150

QY 364 CAGCACCTGCTCTGTAACACCGTTCCGAGAATTCCTGA 405  
Db 149 CAGCACCTGCTCTGTAACACCGTTCCGAGAATTCCTGA 108

RESULT 6  
US-10-806-611-1  
; Sequence 1, Application US/10806611  
; Publication No. US20060159655A1  
; GENERAL INFORMATION:  
; APPLICANT: Collins, Mary  
; APPLICANT: Chin, Elaine Y.  
; APPLICANT: Senates, Mayra  
; APPLICANT: Young, Deborah A.

```

; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
; TITLE OF INVENTION: INTERLEUKIN-21/ INTERLEUKIN-21 RECEPTOR
; FILE REFERENCE: 16158-013001
; CURRENT APPLICATION NUMBER: US 10/806,611
; CURRENT FILING DATE: 2004-03-22
; PRIORITY APPLICATION NUMBER: US 60/456,920
; PRIORITY FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-806-611-1

Query Match          Score 298;  DB 6;  Length 617;
Best Local Similarity 83.8%;  Pred. No. 8.9e-91;
Matches 337;  Conservative 83.8%;  0;  Mismatches 65;  Indels 0;  Gaps 0;
QY
  4 CAAGGTCAGATGCCACATGATTGAGATCGTCACTTAGATATGATATGTTGATCAGTCG 63
Db 134 CAAGGTCAGATGCCACATGATTGAGATCGTCACTTAGATATGATATGTTGATCAGTCG 193
QY
  64 AAAAATTATGTGAAAGTGGACCTGGTCCGGAAATTCTCGCCGCTCGGAAGAGTGTGAGACC 123
Db 194 AAAAATTATGTGAAAGTGGACCTGGTCCGGAAATTCTCGCCGCTCGGAAGAGTGTGAGACC 253
QY
  124 AACCTGTGAGCTGGTCCGGTTCCTCGGTTCAGAAAGGCCAGCTCGAAATCCGCAACACC 183
Db 254 AACCTGTGAGCTGGTCCGGTTCCTCGGTTCAGAAAGGCCAGCTCGAAATCCGCAACACC 313
QY
  184 GGTTACAAAGAACCTATCATCAAGTTCCATTAAGAACCTGAAAGTAACCCGGTCC 243
Db 314 GGAAACAAATGAAAGATAATCACTGATCATTAAGAACCTGAAAGTAACCCGGTCC 373
QY
  244 ACCACAGCAGGGCTGTCTGTCAGAAACGACCGCTGACTGACCTGCGCGCTGTGATCTATGAG 303
Db 374 ACAGATGAGGGAGAGAAGCAAGAACAGACTAACATGCGCTGAGTGTCTATGAG 433
QY
  304 AAAAACCCGCGAAAGAAATTCCTGGAAACGTTCAATCCCTGCGCAGAAATTCAC 363
Db 434 AAACACCAACCCAGAAATTCCTGGAAACGTTCAATCCCTGCGCAGAAATTCAC 493
QY
  364 CAGCAGCTGCTCGTACCCAGCTGAAAGTTCAATCACTTCCTCCAAAGATGATTCA 405
Db 494 CAGCTCTGCTCTAGAACACAGCGAAGTGAAAGTTCCGTA 535

RESULT 7
US-10-806-611-3
; Sequence 3, Application US/10806611
; Publication No. US20060159655A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mary
; APPLICANT: Chin, Elaine Y.
; APPLICANT: Services Mayra
; APPLICANT: Young, Deborah A.
; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF
; FILE REFERENCE: 16158-013001
; CURRENT APPLICATION NUMBER: US/10/806,611
; PRIORITY APPLICATION NUMBER: US 60/456,920
; PRIORITY FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 3072
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-806-611-3

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QY  
Db  
314 GGAAACGATGAAAGGATATCACTATCAATTAAAGAAACTGAAAGAAACCGCGTC 243  
QY  
244 ACCAAGCAGGTGCGTGTGAGAACGACCGTGTGACTGCTGCCGCGTGTGATCTATGAG 303  
Db  
374 ACAATGTCAGGGAGAGACAGAAACAGACTAACTATGCCTCTATGTTATGAG 433  
QY  
304 AAAAACCGCGAAGAAATTCTGGAACTTCAACTCCGTGCGAAGAAATTCTAC 363  
434 AAAAACCCAAAGAATTCTAGAAAGAAATTCAATCACTTCTCCAAAGATGTTAT 493  
QY  
364 CAGCAGCTGTCTCTGTACCCACCGGTCCGAGGTTCTGA 405  
Db  
494 CAGCTCTGCTCTGAGAACACGGAACTGAAATTCCCTGA 535

RESULT 7  
US-10-806-611-3  
; Sequence 3, Application US/10806611  
; Publication No. US20160159655A1  
; GENERAL INFORMATION:  
; APPLICANT: Collins, Mary  
; APPLICANT: Chin, Blaine Y.  
; APPLICANT: Services, Mayra  
; APPLICANT: Young, Deborah A.  
; TITLE OF INVENTION: TREATING IMMUNOLOGICAL DISORDERS USING AGONISTS OF

Sequence 26, Application US/10735149  
Publication No. US20060134754A1  
GENERAL INFORMATION:  
APPLICANT: Chan, Chung  
APPLICANT: Zamost, Bruce L.  
APPLICANT: Covert, Douglas C.  
APPLICANT: Liu, Hong Y.  
APPLICANT: De Jongh, Karen S.  
APPLICANT: Meyer, Jeffrey D.  
APPLICANT: Holzerman, Susan D.  
TITLE OF INVENTION: VECTORS AND METHODS  
TITLE OF INVENTION: IN A PROKARYOTIC  
FILE REFERENCE: 02-12  
CURRENT APPLICATION NUMBER: US/10/73  
CURRENT FILING DATE: 2003-12-12  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: FastSEQ for Windows Version  
SEQ ID NO 26  
LENGTH: 64  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligonucleotide  
US-10-735-149-26

TITLE OF INVENTION: INTERLEUKIN-21/INTERLEUKIN-21 RECEPTOR  
FILE REFERENCE: 16158-013001  
CURRENT APPLICATION NUMBER: US/10/806,611  
CURRENT FILING DATE: 2004-03-22  
PRIORITY APPLICATION NUMBER: US 60/456,920  
PRIORITY FILING DATE: 2003-03-21  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3  
LENGTH: 3072  
TYPE: DNA  
ORGANISM: *Mus musculus*  
US-10-806-611-3

Query Match 44.9%; Score 182; DB 6; Length 3072;

US-10-735-149-25/c  
; Sequence 25, Application US/10735149  
; Publication No. US20060134754A1  
; GENERAL INFORMATION:  
; APPLICANT: Chan, Chung  
; APPLICANT: Zamost, Bruce L.  
; APPLICANT: Covert, Douglas C.  
; APPLICANT: Liu, Hong Y.  
; APPLICANT: De Jongh, Karen S.  
; APPLICANT: Meyer, Jeffrey D.  
; APPLICANT: Holderman, Susan D.  
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21  
; TITLE OF INVENTION: IN A PROKARYOTIC HOST  
; FILE REFERENCE: 02-12  
; CURRENT APPLICATION NUMBER: US/10/735,149  
; CURRENT FILING DATE: 2003-12-12  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 25  
; LENGTH: 63  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide ZC40133  
; US-10-735-149-25

RESULT 10  
Query Match 15.6%; Score 63; DB 6; Length 63;  
Best Local Similarity 100.0%; Pred. No. 1.6e-11; Mismatches 0; Indels 0; Gaps 0;  
Matches 63; Conservative 0; MisMatches 0; Del 0; Insert 0; Gap 0;  
Db 63  
Qy 58 CAGCTGAAATTATGTTGAAAGCTGGATTCCGGAAATTCTGCGCGCTCGGAAAGATTT 117  
Db 63 CAGCTGAAATTATGTTGAAAGCTGGATTCCGGAAATTCTGCGCGCTCGGAAAGATTT 4

Qy 118 GAG 120  
Db 3 GAG 1

RESULT 11  
US-10-735-149-18  
Query Match 14.8%; Score 60; DB 6; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1.6e-10; Mismatches 0; Indels 0; Gaps 0;  
Matches 60; Conservative 0; MisMatches 0; Del 0; Insert 0; Gap 0;  
Db 60  
Qy 110 AGAGCTTGAGGACCACTGAGTGGTCCGCTTCTCTGAGAAAGCCAGCTGA 169  
Db 60 AGAGCTTGAGGACCACTGAGTGGTCCGCTTCTCTGAGAAAGCCAGCTGA 1

RESULT 12  
US-10-735-149-19/c  
; Sequence 19, Application US/10735149  
; Publication No. US20060134754A1  
; GENERAL INFORMATION:  
; APPLICANT: Chan, Chung  
; APPLICANT: Zamost, Bruce L.  
; APPLICANT: Covert, Douglas C.  
; APPLICANT: Liu, Hong Y.  
; APPLICANT: De Jongh, Karen S.  
; APPLICANT: Meyer, Jeffrey D.  
; APPLICANT: Holderman, Susan D.  
; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21  
; TITLE OF INVENTION: IN A PROKARYOTIC HOST  
; FILE REFERENCE: 02-12  
; CURRENT APPLICATION NUMBER: US/10/735,149  
; CURRENT FILING DATE: 2003-12-12  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 19  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide ZC22967  
; US-10-735-149-19

Query Match 14.8%; Score 60; DB 6; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1.6e-10; Mismatches 0; Indels 0; Gaps 0;  
Matches 60; Conservative 0; MisMatches 0; Del 0; Insert 0; Gap 0;  
Db 60  
Qy 110 AGAGCTTGAGGACCACTGAGTGGTCCGCTTCTCTGAGAAAGCCAGCTGA 169  
Db 60 AGAGCTTGAGGACCACTGAGTGGTCCGCTTCTCTGAGAAAGCCAGCTGA 1

RESULT 13

US-10-735-149-20

; Sequence 20, Application US/10735149

; Publication No. US20060134754A1

; GENERAL INFORMATION:

; APPLICANT: Chan, Chung

; APPLICANT: Zamost, Bruce L.

; APPLICANT: Covert, Douglas C.

; APPLICANT: Liu, Hong Y.

; APPLICANT: De Jongh, Karen S.

; APPLICANT: Meyer, Jeffrey D.

; APPLICANT: Holderman, Susan D.

; APPLICANT: Hojderman, Susan D.

; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21

; TITLE OF INVENTION: IN A PROKARYOTIC HOST

; FILE REFERENCE: 02-12

; CURRENT APPLICATION NUMBER: US/10/735,149

; CURRENT FILING DATE: 2003-12-12

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 20

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: oligonucleotide ZC22968

US-10-735-149-20

Query Match 14.8%; Score 60; DB 6; Length 60; Best Local Similarity 100.0%; Pred. No. 1.6e-10; Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 GAGCGTCGTCGTCGAGAACGCGCTGACTGGCTCTGATGTTCTATGAGAAAAA 309

Db 1 GAGCGTCGTCGAGAACGCGCTGACTGGCTCTGATGTTCTATGAGAAAAA 60

RESULT 14

US-10-735-149-21/C

; Sequence 21, Application US/10735149

; Publication No. US20060134754A1

; GENERAL INFORMATION:

; APPLICANT: Chan, Chung

; APPLICANT: Zamost, Bruce L.

; APPLICANT: Covert, Douglas C.

; APPLICANT: Liu, Hong Y.

; APPLICANT: De Jongh, Karen S.

; APPLICANT: Meyer, Jeffrey D.

; APPLICANT: Holderman, Susan D.

; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21

; TITLE OF INVENTION: IN A PROKARYOTIC HOST

; FILE REFERENCE: 02-12

; CURRENT APPLICATION NUMBER: US/10/735,149

; CURRENT FILING DATE: 2003-12-12

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 21

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: oligonucleotide ZC22969

US-10-735-149-21

Query Match 14.8%; Score 60; DB 6; Length 60; Best Local Similarity 100.0%; Pred. No. 1.6e-10; Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 GTGATTCCTATGAGAAACCGCGAAAGATAATTCTGGAAAGTTCATCCCTGCTGC 349

Db 60 GTGATTCCTATGAGAAACCGCGAAAGATAATTCTGGAAAGTTCATCCCTGCTGC 1

RESULT 15

US-10-735-149-22

; Sequence 22, Application US/10735149

; Publication No. US20060134754A1

; GENERAL INFORMATION:

; APPLICANT: Chan, Chung

; APPLICANT: Zamost, Bruce L.

; APPLICANT: Covert, Douglas C.

; APPLICANT: Liu, Hong Y.

; APPLICANT: De Jongh, Karen S.

; APPLICANT: Meyer, Jeffrey D.

; APPLICANT: Holderman, Susan D.

; APPLICANT: Hojderman, Susan D.

; TITLE OF INVENTION: VECTORS AND METHODS FOR PRODUCING IL-21

; TITLE OF INVENTION: IN A PROKARYOTIC HOST

; FILE REFERENCE: 02-12

; CURRENT APPLICATION NUMBER: US/10/735,149

; CURRENT FILING DATE: 2003-12-12

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 22

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: oligonucleotide ZC22970

US-10-735-149-22

Query Match 14.8%; Score 60; DB 6; Length 60; Best Local Similarity 100.0%; Pred. No. 1.6e-10; Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 330 ACGTTCAAATCCCTGCTGAGAAATTCACCAAGGACCTGCTCTCGTACCCAGGG 389

Db 1 ACGTTCAAATCCCTGCTGAGAAATTCACCAAGGACCTGCTCTCGTACCCAGGG 60

Search completed: August 7, 2006, 14:03:08  
Job time : 1538 secs

Copyright (C) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2006, 12:03:42 ; Search time 2686 Seconds  
(without alignment(s))  
9642.109 Million cell updates/sec

Title: US-10-735-149-27

Perfect score: 405

Sequence: 1 atgcggatccaaatcgcca. .... acgggtccggaaatccgtga 405

Scoring table: IDENTITY\_NUC Gap10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenBank:  
1: gb\_env:  
2: gb\_pac:  
3: gb\_ph:  
4: gb\_pl:  
5: gb\_pr:  
6: gb\_ro:  
7: gb\_sts:  
8: gb\_sy:  
9: gb\_un:  
10: gb\_vl:  
11: gb\_ov:  
12: gb\_hdg:  
13: gb\_in:  
14: gb\_om:  
15: gb\_ba:  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	299.6	74.0	483	AR174605
2	299.6	74.0	483	BD248998
3	299.6	74.0	483	AR374097
4	299.6	74.0	483	AR456247
5	299.6	74.0	489	DD180237
6	299.6	74.0	564	BC066260
7	299.6	74.0	566	BC066258
8	299.6	74.0	566	BC066261
9	299.6	74.0	566	BC066262
10	299.6	74.0	642	AR174547
11	299.6	74.0	642	BD248940
12	299.6	74.0	642	CS034091
13	299.6	74.0	642	CS036718
14	299.6	74.0	642	CS043043
15	299.6	74.0	642	CS045670
16	299.6	74.0	642	CS080568
17	299.6	74.0	642	CS237050
18	299.6	74.0	642	AR374039

ALIGNMENTS

Result No.	Score	Match Length	DB ID	Description
1	299.6	74.0	483	AR174605 Sequence
2	299.6	74.0	483	BD248998 Novel cyt
3	299.6	74.0	483	AR374097 Sequence
4	299.6	74.0	483	AR456247 Sequence
5	299.6	74.0	489	DD180237 Albumin P
6	299.6	74.0	564	BC066260 Homo sapi
7	299.6	74.0	566	BC066258 Homo sapi
8	299.6	74.0	566	BC066261 Homo sapi
9	299.6	74.0	566	BC066262 Homo sapi
10	299.6	74.0	642	AR174547 Sequence
11	299.6	74.0	642	BD248940 Novel cyt
12	299.6	74.0	642	CS034091 Sequence
13	299.6	74.0	642	CS036718 Sequence
14	299.6	74.0	642	CS043043 Sequence
15	299.6	74.0	642	CS045670 Sequence
16	299.6	74.0	642	CS080568 Sequence
17	299.6	74.0	642	CS237050 Sequence
18	299.6	74.0	642	AR374039 Sequence

RESULT 1

AR174605

LOCUS AR174605

DEFINITION Sequence 63 from patent US 6307024.

ACCESSION AR174605

VERSION AR174605.1

KEYWORDS GI:17914925

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 483)

AUTHORS Novak,J.E., Presnell,S.R., Speicher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.

JOURNAL Cytokine zalphaII ligand

TITLE Patent: US 6307024-A 63-23-OCT-2001;

FEATURES Location/Qualifiers

source

ORIGIN

Query Match 74.0% ; Score 299.6; DB 2; Length 483;

Best Local Similarity 84.1%; Prey. No. 3.7e-92;

Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAAGGTCAAGATGCCACATGATTAGATGAAATGCCAACATATGATATGTTGATCAGCTG 63

Db 82 CAAAGGTCAAGATGCCACATGATTAGATGAAATGCCAACATATGATATGTTGATCAGCTG 141

QY 64 AAAAATATGTTGATGACCTGCTGCCGAAATTCCTGCGGCCGAGATGTTGAGAC 123

Db 142 AAATATGTTGATGACTTGTGCTCCCTGAATTCTGCGCACTGAGATGTTGAGAC 201

QY 124 ACTGTGATGTTGCTCGCTTCTCCCTGTTCCGAAAGCCACGCTGAATCCGAAACCC 183

Db 202 ACTGTGATGTTGCTCGCTTCTCCCTGTTCCGAAAGCCACGCTGAATCCGAAACCC 261

QY 184 GCTAACACGAACTATCATCACGTTCCATTAAGAACCTAACGAAACGCGCTCC 243

Db 262 GAAACATGAAAGGATATCATGATCAATTAAGAGCTGAGAGGAACACCTTC 321

QY	244	ACRAACGAGGTCTCTGTCGAAACACCTCTGACTGCGGTCCTGAG 303	Db
Db	322	ACAAATGCGAGGAGAGACGAGAACACAGACTAACATGCCTCTATGAG 381	QY
QY	304	AAAAACCCGAAAGAATTCCCGAACCTTCGACCTTCAGATCCCTGCTGAGAAATCTCAC 363	Db
Db	382	AAAAACCCGAAAGAATTCCCGAACCTTCGACCTTCAGATCCCTGCTGAGAAATCTCAC 441	QY
QY	364	CAGCACCTGCTCGTACCGGTCCGAAAGTTCTGA 405	Db
Db	442	CAGCATCTGCTCTAGAACACAGGAAGTGAAGATTCCTGA 483	QY
RESULT 2	BD248998		
LOCUS	BD248998		
DEFINITION	Novel cytokine ZALPHALL ligand.	483 bp	DNA
ACCESSION	BD248998		linear
VERSION	BD248998.1	GI:33058768	PAT 17-JUL-2003
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo		
REFERENCE	Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.	1 (bases 1 to 483)	
AUTHORS	Novel cytokine ZALPHALL ligand		
TITLE	Patent: JP 2002537839-A 59 12-NOV-2002;		
JOURNAL	ZYMOGENETICS INC		
COMMENT	OS Homo sapiens (human)		
OS	Homo sapiens (human)		
PN	JP 2002537839-A/59		
PD	12-NOV-2002		
PP	09-MAR-2000 JP 20000503382		
PR	09-MAR-1999 US 60/14203	09/265992 PR	
PR	09-MAR-1999 US 60/14203	09/265992 PR	
PR	01-JUN-1999 US 60/14203	09/265992 PR	
PI	JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHER,DONALD C PI		
PI	RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON, STACEY R DILTON,ANGELA K HAMMOND		
PC	C12N1/09,A61K38/00,A61K45/00,A61P35/00,A61P37/00,C07K14/52, C07K14/53,C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC		
PC	C12N1/21,C12N5/10,C12P21/02,C12P21/02,601N33/53,C12N5/00, PC		
PC	A61K37/02		
CC	Novel cytokine ZALPHALL ligand		
FH	source	1. 483	
FT	location/Qualifiers	/organism='Homo sapiens (human) '.	
FEATURES			
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	/mol_type="genomic DNA"	/ab_xref="Taxon:9606"	
ORIGIN			
Query Match	74.0%	Score 299.6;	DB 2;
Best Local Similarity	84.1%	Pred. No. 3.7e-92;	Length 483;
Matches	338;	Conservative	
	0;	Mismatches	64;
		Indels	0;
		Gaps	0;
QY	4	CAAGGTCAAGATCCGACATGATAGAATGGTCGTCACTATAGATATGTTGATCAGTG	63
Db	82	CAGGTCAAGATCCGACATGATAGAATGGTCGTCACTATAGATATGTTGATCAGTG	141
QY	64	AAAATTATGTTGATGACTCTGTTCCGGAATGGATGTTGAGACCG 123	Db
Db	142	AAAATTATGTTGATGACTCTGTTCCGGAATGGATGAGACCG 201	
QY	124	ACTGTGAGTGTGCGCTTCCTGTTGAGGCCACTAACTGAAAC 183	
Db	202	ACTGTGAGTGTGCGCTTCCTGTTGAGGCCACTAACTGAAAC 261	
QY	184	GTTACAACGAGCTTCACTGTTCAATTAAAGCTGAAAGGAAAC 243	
Db	262	GAAACAATGAGGAGAACACAGACTAACATGCCTCTATGAG 321	
QY	244	ACCAACGAGGTCTGTCGAGAACACCTCTGACCTGCGCTCTGATCTATGAG 303	
Db	322	ACAAATGCGAGGAGAACACAGACTAACATGCCTCTATGAG 381	
QY	304	AAAACCCGAAAGAATTCTCGAACCTTCAACTCCCTGCTGAGAAATCTCAC 363	
Db	382	AAAACCCGAAAGAATTCTCGAACCTTCAACTCCCTGCTGAGAAATCTCAC 441	
QY	364	CAGCACCTGCTCTAGAACACAGGAAGTGAAGATTCCTGA 405	
Db	442	CAGCATCTGCTCTAGAACACAGGAAGTGAAGATTCCTGA 483	



REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo
AUTHORS	1 (bases 1 to 564)
COLLINS FS, REINGOLD EA, GROUSE LH, DERGE JG, KLAUSSNER RD, STRAUSBERG RL, BUETOW KH, SCHAEFER CF, BHAT NK, HOPKINS RF, JORDAN H, MOORE T, MAX SI, WANG J, HSIEH L, STAPLETON M, SOARES MB, BONALDO MF, CASAVANT TL, GM, HONG L, DIATCHENKO L, MARUSSINA K, FARMER AA, RUBIN B, SCHEETZ TE, BROWNSTEIN MJ, USDIN TB, TOSHIYUKI S, CARNINCI P, PRANGE C, RAHA SS, LOQUELLANO NA, PETERS GJ, ABRAMSON RD, MULLAHY SJ, BOSAK SA, MCEWAN PJ, MCKERNAN KJ, MALEK JA, GUNARATNE PH, RICHARDS S, WORLEY KC, HALE S, GARCIA AM, GAY LJ, HULKY SW, VILLALON DK, MUZNY DM, SODERBERG RJ, LU X, GIBBS RA, FAHEY J, HELTON E, KETTERMAN M, MADAN A, RODRIGUEZ S, SANCHEZ A, WHITING M, MADAN A, YOUNG AC, SHEVCHENKO Y, BOUFFARD GG, BLAKESLEY RW, TOUCHMAN JW, GREEN BD, DICKSON MC, RODRIGUEZ AC, GRIMWOOD J, SCHMITZ J, MYERS RM, BUTTERFIELD VS, KRYWIENSKI MJ, SKALSKA U, SMALIUS DE, SCHNEICH A, SCHEIN JE, JONES SJ and MARA MA.	
CONSRM	Mammalian Gene Collection Program Team
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBLISHED	1247932
REFERENCE	2 (bases 1 to 564)
AUTHORS	Director MGC Project.
COMMENT	Direct Submission
JOURNAL	Submitted (03-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
CONTACT	NIH-MGC Project URL: <a href="http://mgc.ncbi.nlm.nih.gov">http://mgc.ncbi.nlm.nih.gov</a>
EMAIL	cgbabs-r@mail.nih.gov
TISSUE	Procurement: Narayan Bhat
PROCUREMENT	CDNA Library Preparation: Bhar Laboratory
CDNA	Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
WEBSITE	<a href="http://www-bhgc.stanford.edu">http://www-bhgc.stanford.edu</a>
CONTACT	(Dickson, Mark) mcd@axil.stanford.edu
DICKSON	M., SCHMITZ, J., GRIMWOOD, J., RODRIGUEZ, A., and MYERS, R. M.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>
SOURCE	This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11141874.
LOCATION	Location/Qualifiers
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/tissue type="PCR rescued clones".	
/clone_libr="NIH MGC_195"	
/lab_host="DH10B"	
/note="Vector: pDNR-Dual"	
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/genes="IL21"	
/note="synonyms: Zail, IL-21"	
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/db_xref="MIM:605384"	
CDS	codon_start=1
REFERENCE	Query Match Best Local Similarity 74.0%; Score 299.6; DB 5; Length 564; Matches 338; Conservative 84.1%; Pred. No. 3 8e-92; 0; Mismatches 64; Indels 0; Gaps 0; Gaps 0;
AUTHORS	4 CAAAGTCAGATGCCACATGATTAGATGATGCCAACATATGATATGTTATCACCTG 63
COLLINS FS, REINGOLD EA, GROUSE LH, DERGE JG, KLAUSSNER RD, STRAUSBERG RL, BUETOW KH, SCHAEFER CF, BHAT NK, HOPKINS RF, JORDAN H, MOORE T, MAX SI, WANG J, HSIEH L, STAPLETON M, SOARES MB, BONALDO MF, CASAVANT TL, GM, HONG L, DIATCHENKO L, MARUSSINA K, FARMER AA, RUBIN B, SCHEETZ TE, BROWNSTEIN MJ, USDIN TB, TOSHIYUKI S, CARNINCI P, PRANGE C, RAHA SS, LOQUELLANO NA, PETERS GJ, ABRAMSON RD, MULLAHY SJ, BOSAK SA, MCEWAN PJ, MCKERNAN KJ, MALEK JA, GUNARATNE PH, RICHARDS S, WORLEY KC, HALE S, GARCIA AM, GAY LJ, HULKY SW, VILLALON DK, MUZNY DM, SODERBERG RJ, LU X, GIBBS RA, FAHEY J, HELTON E, KETTERMAN M, MADAN A, RODRIGUEZ S, SANCHEZ A, WHITING M, MADAN A, YOUNG AC, SHEVCHENKO Y, BOUFFARD GG, BLAKESLEY RW, TOUCHMAN JW, GREEN BD, DICKSON MC, RODRIGUEZ AC, GRIMWOOD J, SCHMITZ J, MYERS RM, BUTTERFIELD VS, KRYWIENSKI MJ, SKALSKA U, SMALIUS DE, SCHNEICH A, SCHEIN JE, JONES SJ and MARA MA.	
CONSRM	Mammalian Gene Collection Program Team
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBLISHED	1247932
REFERENCE	2 (bases 1 to 566)
ORIGIN	LRRKPPSTNAGRKRHLTCPSDCSVEKKPPRFELRKPSLILQKRIHOHLSRTHSE D5"
RESULT	7
BC066258	BC066258
LOCUS	Homo sapiens intereleukin 21, mRNA (cDNA clone MGC:79376
DEFINITION	IMAGE:6971861), complete cds.
ACCESSION	BC066258
VERSION	BC066258.1
KEYWORDS	GI:42542658 MGC.
SOURCE	Homo sapiens (human)
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo
REFERENCE	1 (bases 1 to 566)
AUTHORS	1 (bases 1 to 566)
COLLINS FS, REINGOLD EA, GROUSE LH, DERGE JG, KLAUSSNER RD, STRAUSBERG RL, BUETOW KH, SCHAEFER CF, BHAT NK, HOPKINS RF, JORDAN H, MOORE T, MAX SI, WANG J, HSIEH L, STAPLETON M, SOARES MB, BONALDO MF, CASAVANT TL, GM, HONG L, DIATCHENKO L, MARUSSINA K, FARMER AA, RUBIN B, SCHEETZ TE, BROWNSTEIN MJ, USDIN TB, TOSHIYUKI S, CARNINCI P, PRANGE C, RAHA SS, LOQUELLANO NA, PETERS GJ, ABRAMSON RD, MULLAHY SJ, BOSAK SA, MCEWAN PJ, MCKERNAN KJ, MALEK JA, GUNARATNE PH, RICHARDS S, WORLEY KC, HALE S, GARCIA AM, GAY LJ, HULKY SW, VILLALON DK, MUZNY DM, SODERBERG RJ, LU X, GIBBS RA, FAHEY J, HELTON E, KETTERMAN M, MADAN A, RODRIGUEZ S, SANCHEZ A, WHITING M, MADAN A, YOUNG AC, SHEVCHENKO Y, BOUFFARD GG, BLAKESLEY RW, TOUCHMAN JW, GREEN BD, DICKSON MC, RODRIGUEZ AC, GRIMWOOD J, SCHMITZ J, MYERS RM, BUTTERFIELD VS, KRYWIENSKI MJ, SKALSKA U, SMALIUS DE, SCHNEICH A, SCHEIN JE, JONES SJ and MARA MA.	
CONSRM	Mammalian Gene Collection Program Team
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBLISHED	1247932
REFERENCE	2 (bases 1 to 566)

AUTHORS	Director: MGC Project.
TITLE	Direct Submission
JOURNAL	Submitted (03-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgapbs@mail.nih.gov">cgapbs@mail.nih.gov</a>
Tissue Procurement	Narayan Bhat
CDNA Library Preparation	Bhat Laboratory
DNA Sequencing	Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site	<a href="http://www-shgc.stanford.edu">http://www-shgc.stanford.edu</a>
Contract	(Dickson, Mark) <a href="mailto:mcd@paxil.stanford.edu">mcd@paxil.stanford.edu</a>
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.	
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>
source	Series: IRAX plate: 172 Row: d Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11141874.
Location/Qualifiers	
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/clone_id="NIH_MGC_195"	
/lab_host="DRI10B"	
/note="vector: pdNR-Dual"	
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/gene="IL21"	
/note="synonyms: zail1, IL-21"	
/db_xref="GeneID:59067"	
/db_xref="MIM:605384"	
46 .534	
/gene="IL21"	
/codon_start=1	
/product="interleukin 21"	
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LKRKPPTSTNAGRRQRKHLTCPSCDSYKKPKFELFRKSLQRMHQLSSRTHGSE	
DS"	
ORIGIN	
Query Match	
Best Local Similarity 74.0%; Score 299.6; DB 5; Length 566;	
Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;	
4 CAAAGTCAGATGCCACATGATTAGCTGGTCACATTAGTAGATCTGTTGAGCTG 63	
133 CAAGCTTCAAGATGCCACATGATTAGCTGGTCACATTAGATCTGTTGAGCTG 192	
64 AAAATATATGTTGATGACCTGGTCCGGAAATCTGGCCGACTCCGGAGATGTGAGCC 123	
193 AAAATATATGTTGATGACCTGGTCCGGAAATCTGGCCGACTCCGGAGATGTGAGCC 252	
124 AACTGTGAGTGGTCAGCTTCTCTTTCAGAAGGCCAACTAAGTCAGCAATACA 183	
253 AACTGTGAGTGGTCAGCTTCTCTTTCAGAAGGCCAACTAAGTCAGCAATACA 312	
184 GGTGACACAGGAACTCTATCAACGTTTCATTAAGAAACTGAAACGTTAACCCGTC 243	
313 GGAAACATGAGAGGATATCAATGATTAAGTGTGAGAGGAAACCCCTCC 372	
REMARK	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>
COMMENT	This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11141874.
AUTHORS	Director: MGC Project.
TITLE	Direct Submission
JOURNAL	Submitted (03-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgapbs@mail.nih.gov">cgapbs@mail.nih.gov</a>
Tissue Procurement	Narayan Bhat
CDNA Library Preparation	Bhat Laboratory
DNA Sequencing	Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site	<a href="http://www-shgc.stanford.edu">http://www-shgc.stanford.edu</a>
Contract	(Dickson, Mark) <a href="mailto:mcd@paxil.stanford.edu">mcd@paxil.stanford.edu</a>
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.	
RESULT	8
BC066261	BC066261
LOCUS	Homo sapiens interleukin 21, mRNA (cDNA clone MGC:79379 IMAGE:6971865), complete cds.
DEFINITION	
VERSION	BC066261.1 GI:42542656
KEYWORDS	MGC
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.	
REFERENCE	1 (bases 1 to 566)
AUTHORS	Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shemesh CM, Schuler GD, Altechall SF, Zeeberg BR, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Schetetz TE, Brownstein MJ, Uddin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loqueline NA, Peters GJ, Abramson RD, Miliyah SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Morley KC, Hale S, Garcia AW, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergren BJ, Lu X, Gibbs RA, Fahney J, Helton B, Kettman M, Madan A, Rodriguez S, Sanchez A, Whiting M, Madan A, Young AC, Shvchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Salzberg SL, Smilis DE, Schnetrich A, Schein JE, Jones SJ and Marra MA.
CONTRM	Mammalian Gene Collection Program Team
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
POUNDED	1247932
REFERENCE	2 (bases 1 to 566)
AUTHORS	Director: MGC Project.
TITLE	Direct Submission
JOURNAL	Submitted (03-FEB-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgapbs@mail.nih.gov">cgapbs@mail.nih.gov</a>
Tissue Procurement	Narayan Bhat
CDNA Library Preparation	Bhat Laboratory
DNA Sequencing	Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site	<a href="http://www-shgc.stanford.edu">http://www-shgc.stanford.edu</a>
Contract	(Dickson, Mark) <a href="mailto:mcd@paxil.stanford.edu">mcd@paxil.stanford.edu</a>
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.	
REMARK	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>
COMMENT	This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11141874.



ORIGIN	DS"
Query Match	74.0%; Score 299.6; DB 5; Length 566;
Best Local Similarity	84.1%; Pred. No. 3.8e-92; Mismatches 64; Indels 0; Gaps 0;
Matches	338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy	4 CAAAGTCAGTCAGTCGCACATGATAGATAGTGTGATCAGTC 63
Db	134 CAAGTCAGTCAGTCGCACATGATAGATAGTGTGATCAGTC 193
Qy	64 AAAATTATGTGATGACTGTCGCTGAAAGCCAGTCGAATCGCAACACC 123
Db	194 AAAATTATGTGATGACTGTCGCTGAAATTCGCAAGTCGAATCGCAACACC 253
Qy	124 ACTGTGAGTGCTCCGCTTCTCTGGAACTCTCGGAGTGTGAGACC 183
Db	193 AAAATTATGTGATGACTGTCGCTGAAATTCGCAAGTCGAATCGCAACACC 252
Qy	124 ACTGTGAGTGCTCCGCTTCTCTGGAACTCTCGGAGTGTGAGACC 183
Db	253 ACTGTGAGTGCTCCGCTTCTCTGGAACTCTCGGAGTGTGAGACC 312
Qy	184 CGTAAACAGCAGTCATCACTAACGTTCTAAAGACTGAAACGTTAACCGCGTCC 243
Db	313 GGAACACATGAAAGGATAATCAATGATCATTAAGGAGGAAACCTTCC 372
Qy	244 ACCAAGCAGTCGCTGCGAAGACCGCTGACTCTGGCGCTCTGATCTAG 303
Db	373 ACAAATGCAAGGAGAAACAGACAGACTAACATGCCCTCATGTGATTCTAG 432
Qy	304 AAAAACCGCGAAAGATTCCTGGAACTGTTCAAACTCCCTGCTGAGAAATGATCAC 363
Db	433 AAAAACCGCGAAAGATTCCTGGAACTGTTCAAACTCCCTGCTGAGAAATGATCAC 492
Qy	364 CAGCACCTGCTCTGTGACCCACGTTCCGAGATCTCTGAAAGATGATCAC 405
Db	493 CAGCATCTGCTCTAGAACACACGGAGTCAGATCTCTGAAAGATGATCAC 534
RESULT 10	
AR174547	
LOCUS	AR174547 AR174547 Sequence 1 from patent US 6307024. DNA linear
DEFINITION	PAT 17-DEC-2001
ACCESSION	AR174547 AR174547.1 GI:17914867
VERSION	
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 642)
AUTHORS	Novak,J.B., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.
TITLE	Novel cytokine ZALPHA11 ligand
JOURNAL	Patent: JP 200257839-A 1 12-NOV-2002;
COMMENT	ZMOGENETICS INC
OS	Homo sapiens (human)
PN	JP 200257839-A/1
PD	12-NOV-2002
PR	09-MAR-2000 JP 20000603382
PR	09-MAR-1999 US 09/264908, 11-MAR-1999 US 09/265992 PR
PR	01-JUL-1999 US 60/142013
PI	JULIA E NOVAK, SCOTT R PRESNELL, CINDY A SPRECHER, DONALD C PI
FOSTER,	RICHARD D HOLLY JANE A GROSS, JANET V JOHNSTON, ANDREW J NELSON, PI
PI	SPACER R DILION ANGELA K HAMMOND, PI
PC	C12N15/09, A61K36/00, A61K45/00, A61P35/00, A61P37/00, C07K14/52, C07K14/53, C07K14/54, C07K14/55, C07K15/24, C07K19/00, C12N1/15, C12N1/19, PC
PC	C12N1/21, C12N5/10, C12P21/02, C12P21/02, G01N33/53, C12N15/00, C12N5/00, PC
PC	A61K37/02
CC	Novel cytokine ZALPHA11 ligand
FT	Key
FT	Location/Qualifiers
FEATURES	1. .642
source	/organism="unknown"
ORIGIN	/mol_type="unassigned DNA"
Query Match	74.0%; Score 299.6; DB 2; Length 642;
Best Local Similarity	84.1%; Pred. No. 4e-92; Mismatches 64; Indels 0; Gaps 0;
Matches	338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy	4 CAAAGTCAGTCAGTCGCACATGATAGATAGTGTGATCAGTC 63
Db	134 CAAGTCAGTCAGTCGCACATGATAGATAGTGTGATCAGTC 193
Qy	64 AAAATTATGTGATGACTGTCGCTGAAAGCCAGTCGAATCGCAACACC 123
Db	194 AAAATTATGTGATGACTGTCGCTGAAATTCGCAAGTCGAATCGCAACACC 253
Qy	124 ACTGTGAGTGCTCCGCTTCTCTGGAACTCTCGGAGTGTGAGACC 183
Db	254 ACTGTGAGTGCTCCGCTTCTCTGGAACTCTCGGAGTGTGAGACC 313
RESULT 11	
BD248940	
LOCUS	BD248940 Novel cytokine ZALPHA11 ligand.
DEFINITION	
ACCESSION	BD248940
VERSION	BD248940.1 GI:31058710
KEYWORDS	JP 2002537839-A/1
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Earchontoglires; Primates; Catarrhini;
REFERENCE	1 (bases 1 to 642)
AUTHORS	Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.
TITLE	Novel cytokine ZALPHA11 ligand
JOURNAL	Patent: JP 200257839-A 1 12-NOV-2002;
COMMENT	ZMOGENETICS INC
OS	Homo sapiens (human)
PN	JP 200257839-A/1
PD	12-NOV-2002
PR	09-MAR-2000 JP 20000603382
PR	09-MAR-1999 US 09/264908, 11-MAR-1999 US 09/265992 PR
PR	01-JUL-1999 US 60/142013
PI	JULIA E NOVAK, SCOTT R PRESNELL, CINDY A SPRECHER, DONALD C PI
FOSTER,	RICHARD D HOLLY JANE A GROSS, JANET V JOHNSTON, ANDREW J NELSON, PI
PI	SPACER R DILION ANGELA K HAMMOND, PI
PC	C12N15/09, A61K36/00, A61K45/00, A61P35/00, A61P37/00, C07K14/52, C07K14/53, C07K14/54, C07K14/55, C07K15/24, C07K19/00, C12N1/15, C12N1/19, PC
PC	C12N1/21, C12N5/10, C12P21/02, C12P21/02, G01N33/53, C12N15/00, C12N5/00, PC
PC	A61K37/02
CC	Novel cytokine ZALPHA11 ligand
FT	Key
FT	Location/Qualifiers
FEATURES	1. .642
source	/organism="homo sapiens"
ORIGIN	/mol_type="genomic DNA"
Query Match	74.0%; Score 299.6; DB 2; Length 642;
Best Local Similarity	84.1%; Pred. No. 4e-92; Mismatches 64; Indels 0; Gaps 0;
Matches	338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy	4 CAAAGTCAGTCAGTCGCACATGATAGATAGTGTGATCAGTC 63
Db	134 CAAGTCAGTCAGTCGCACATGATAGATAGTGTGATCAGTC 193
Qy	64 AAAATTATGTGATGACTGTCGCTGAAAGCCAGTCGAATCGCAACACC 123
Db	194 AAAATTATGTGATGACTGTCGCTGAAATTCGCAAGTCGAATCGCAACACC 253
Qy	124 ACTGTGAGTGCTCCGCTTCTCTGGAACTCTCGGAGTGTGAGACC 183
Db	254 ACTGTGAGTGCTCCGCTTCTCTGGAACTCTCGGAGTGTGAGACC 123

Db	194	AAAATTATGTTGAACTGACTTGTGCCCCCTGAAATTCTGCCCCAGTCAGAAGATGAGACA	253	Db	434	AAAAACACCCAAAGAATTCTAGAAGATTAATCACTTCTCCAAAGATGATTAT	493
Oy	124	ACTGTGAGTGTGCGCTTCTCTGTGTCAGAAAGCCGAACTCCCTGACTGCGCTCTGAGATCTTGTAG	183	Oy	354	CACACCTGTCCTCTGTCACCCACGGTCCGGAGATTCCTGA	405
Db	254	ACTGTGAGTGTGCGCTTCTCTGTGTCAGAAAGCCGAACTCCCTGACTGCGCTCTGAGATCTTGTAG	183	Db	434	CAACATCTGTCCTGAGACACGGAGTGTGAGATTCCTGA	535
Oy	184	GTTRACACAGGAACTATCATCAAGTTCCATTAAAGACTGAACGTAACCCCGTCC	243				
Db	314	GGAAACAAATGAAAGGATAATCATGTTCTGAAACAGGAAACACCCACCTGACTGCGCTCTGAGATCTTGTAG	373				
Oy	244	ACCAACAGGAGGAAAGATCTCTGAACTGCTCAATCTCTGAGATTCCTGA	405				
Db	374	ACAAATGCGAGAGACAGAACAGAACACTAACGCTCTGAGATTCCTGA	433				
Oy	184	GTTRACACAGGAACTATCATCAAGTTCCATTAAAGACTGAACGTAACCCCGTCC	243				
Db	314	GGAAACAAATGAAAGGATAATCATGTTCTGAAACAGGAAACACCCACCTGACTGCGCTCTGAGATCTTGTAG	373				
Oy	244	ACCAACAGGAGGAAAGATCTCTGAACTGCTCAATCTCTGAGATTCCTGA	405				
Db	374	ACAAATGCGAGAGACAGAACAGAACACTAACGCTCTGAGATTCCTGA	433				
Oy	304	AAAAACACCCAAAGAATTCTGAGATTCCTGAGACACGGAGTGTGAGATTCCTGA	535				
RESULT 12							
CS034091	CS034091	Sequence 3597 from Patent WO2005016962.	DNA	linear	PAT	10-MAR-2005	
DEFINITION							
ACCESSION	CS034091						
VERSION	CS034091.1	GI:60732828					
KEYWORDS							
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.						
AUTHORS	Abbas, A., Clark, H., Ouyang, W., Williams, M.P., Wood, W.I. and Wu, T.D.						
TITLE	Compositions and methods for the treatment of immune related diseases						
JOURNAL	Patent: WO 2005016962-A 6224 24-FEB-2005; Genentech, Inc. (US)						
FEATURES	Location/Qualifiers						
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Best Local Similarity	74.0%; Score 299.6; DB 2; Length 642;						
Matches	338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
REFERENCE	Abbas, A., Clark, H., Ouyang, W., Williams, M.P., Wood, W.I. and Wu, T.D.						
AUTHORS	Abbas, A., Clark, H., Ouyang, W., Williams, M.P., Wood, W.I. and Wu, T.D.						
TITLE	Compositions and methods for the treatment of immune related diseases						
JOURNAL	Patent: WO 2005016962-A 3597 24-FEB-2005; Genentech, Inc. (US)						
FEATURES	Location/Qualifiers						
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Db	134	CAAGGTCAAGATGCCACATGATTAGATGGCTCAACTTATAGATATGTTGATCAGCTG	63	Db	134	CAAGGTCAAGATGCCACATGATTAGATGGCTCAACTTATAGATATGTTGATCAGCTG	193
Oy	64	AAAATTATGTTGAACTGACTCTGTTCTGTCAGAACGAGATGGAGATCTGAGAC	123	Oy	64	AAAATTATGTTGAACTGACTCTGTTCTGTCAGAACGAGATGGAGATCTGAGAC	123
Db	194	AAAATTATGTTGAACTGACTCTGTTCTGTCAGAACGAGATGGAGATCTGAGAC	253	Db	194	AAAATTATGTTGAACTGACTCTGTTCTGTCAGAACGAGATGGAGATCTGAGAC	253
Oy	124	ACTGTGAGTGTGCGCTTCTCTGTGTCAGAACTTGTGATCATGTTCTGAGATCTGAG	183	Oy	124	ACTGTGAGTGTGCGCTTCTCTGTGTCAGAACTTGTGATCATGTTCTGAGATCTGAG	183
Db	254	ACTGTGAGTGTGCGCTTCTCTGTGTCAGAACTTGTGATCATGTTCTGAGATCTGAG	183	Db	254	ACTGTGAGTGTGCGCTTCTCTGTGTCAGAACTTGTGATCATGTTCTGAGATCTGAG	183
Oy	184	GTTRACACAGGAACTATCATCAAGTTCCATTAAAGACTGAACGTAACCCCGTCC	243	Oy	184	GTTRACACAGGAACTATCATCAAGTTCCATTAAAGACTGAACGTAACCCCGTCC	243
Db	314	GGAAACAAATGAAAGGATAATCATGTTCTGAAACAGGAAACACCCACCTGACTGCGCTCTGAGATCTTGTAG	373	Db	314	GGAAACAAATGAAAGGATAATCATGTTCTGAAACAGGAAACACCCACCTGACTGCGCTCTGAGATCTTGTAG	373
Oy	64	AAAATTATGTTGAACTGACTCTGTTCTGTCAGAACGAGATGGAGATCTGAGAC	123	Oy	304	AAAATTATGTTGAACTGACTCTGTTCTGTCAGAACGAGATGGAGATCTGAGAC	363
Db	194	AAAATTATGTTGAACTGACTCTGTTCTGTCAGAACGAGATGGAGATCTGAGAC	253	Db	194	AAAATTATGTTGAACTGACTCTGTTCTGTCAGAACGAGATGGAGATCTGAGAC	253
Oy	124	ACTGTGAGTGTGCGCTTCTCTGTGTCAGAACTTGTGATCATGTTCTGAGATCTGAG	183	Oy	124	ACTGTGAGTGTGCGCTTCTCTGTGTCAGAACTTGTGATCATGTTCTGAGATCTGAG	183
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Db	314	GGAAACAAATGAAAGGATAATCATGTTCTGAAACAGGAAACACCCACCTGACTGCGCTCTGAGATCTTGTAG	373	Db	314	GGAAACAAATGAAAGGATAATCATGTTCTGAAACAGGAAACACCCACCTGACTGCGCTCTGAGATCTTGTAG	373
Oy	244	ACCAACAGGAGGAAACTATCATCAAGTTCCATTAAAGACTGAACGTAACCCCGTCC	303	Oy	364	CAGCACCTGCTCTGTCACCCACGGTTCCGGAGATTCCTGA	405
Db	374	ACAAATGCGAGAGACAGAACAGAACACTAACGCTCTGAGATCTTGTAG	433	Db	434	CAGCACCTGCTCTGTCACCCACGGTTCCGGAGATTCCTGA	535
Oy	304	AAAAACACCCAAAGAATTCTCTGAAACACCCACCTGACTGCGCTCTGAGATCTTGTAG	363				
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LOCUS							
DEFINITION							
ACCESSION	CS036718						
VERSION	CS036718.1	GI:60734171					
KEYWORDS							
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.						
AUTHORS	Abbas, A., Clark, H., Ouyang, W., Williams, M.P., Wood, W.I. and Wu, T.D.						
TITLE	Compositions and methods for the treatment of immune related diseases						
JOURNAL	Patent: WO 2005016962-A 6224 24-FEB-2005; Genentech, Inc. (US)						
FEATURES	Location/Qualifiers						
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Query Match	Score 299.6; DB 2; Length 642;						
Best Local Similarity	74.0%; Score 299.6; DB 2; Length 642;						
Matches	338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Oy	4	CAAGCTCAAGATCCACATGATTAGATGGCTCAACTTATAGATATGTTGATCAGCTG	63	Oy	4	CAAGCTCAAGATCCACATGATTAGATGGCTCAACTTATAGATATGTTGATCAGCTG	193
Db	134	CAAGGTCAAGATGCCACATGATTAGATGGCTCAACTTATAGATATGTTGATCAGCTG	63	Db	134	CAAGGTCAAGATGCCACATGATTAGATGGCTCAACTTATAGATATGTTGATCAGCTG	193
Oy	64	AAAATTATGTTGAACTGACTCTGTTCTGTCAGAACGAGATGGAGATCTGAGAC	123	Oy	304	AAAATTATGTTGAACTGACTCTGTTCTGTCAGAACGAGATGGAGATCTGAGAC	363
Db	194	AAAATTATGTTGAACTGACTCTGTTCTGTCAGAACGAGATGGAGATCTGAGAC	253	Db	194	AAAATTATGTTGAACTGACTCTGTTCTGTCAGAACGAGATGGAGATCTGAGAC	253
Oy	124	ACTGTGAGTGTGCGCTTCTCTGTGTCAGAACTTGTGATCATGTTCTGAGATCTGAG	183	Oy	124	ACTGTGAGTGTGCGCTTCTCTGTGTCAGAACTTGTGATCATGTTCTGAGATCTGAG	183
Db	254	ACTGTGAGTGTGCGCTTCTCTGTGTCAGAACTTGTGATCATGTTCTGAGATCTGAG	183	Db	254	ACTGTGAGTGTGCGCTTCTCTGTGTCAGAACTTGTGATCATGTTCTGAGATCTGAG	183
Oy	184	GTTRACACAGGAACTATCATCAAGTTCCATTAAAGACTGAACGTAACCCCGTCC	243	Oy	184	GTTRACACAGGAACTATCATCAAGTTCCATTAAAGACTGAACGTAACCCCGTCC	243
Db	314	GGAAACAAATGAAAGGATAATCATGTTCTGAAACAGGAAACACCCACCTGACTGCGCTCTGAGATCTTGTAG	373	Db	314	GGAAACAAATGAAAGGATAATCATGTTCTGAAACAGGAAACACCCACCTGACTGCGCTCTGAGATCTTGTAG	373
Oy	244	ACCAACAGGAGGAAACTATCATCAAGTTCCATTAAAGACTGAACGTAACCCCGTCC	303	Oy	364	CAGCACCTGCTCTGTCACCCACGGTTCCGGAGATTCCTGA	405
Db	374	ACAAATGCGAGAGACAGAACAGAACACTAACGCTCTGAGATCTTGTAG	433	Db	434	CAGCACCTGCTCTGTCACCCACGGTTCCGGAGATTCCTGA	535
Oy	304	AAAAACACCCAAAGAATTCTCTGAAACACCCACCTGACTGCGCTCTGAGATCTTGTAG	363				
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DEFINITION							
ACCESSION	CS043043						
VERSION	CS043043.1	GI:61850089					
KEYWORDS							

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchoptolires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1. Abbas, A., Clark, H., Ouyang, W., Williams, P.M., Wood, W.I. and Wu, T.D.

AUTHORS

TITLE Compositions and methods for the treatment of immune related diseases

JOURNAL Patent: WO 2005019258 A 3597 03-MAR-2005; Genentech, Inc. (US)

FEATURES Location/Qualifiers

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QY 4 CAAGGTCAGATGCCACATGATTAGATGACTGTCAGTCACTTGTAGATTTGTGATCGTG 63

Db 134 CAAGGTCAGATGCCACATGATTAGATGACTGTCAGTCACTTGTGATCGTG 193

QY 64 AAAATTATGTAATGACTGTGTCGGAACTTCCTGGGGTCCGGAGATGTGAGAC 123

Db 194 AAAATTATGTAATGACTGTGTCGGAACTTCCTGGGGTCCGGAGATGTGAGAC 253

QY 124 ACTGTGAGTGTGTCCTTCCTGTTAGAAGCCGCTGAAATCGCAAACACC 183

Db 254 ACTGTGAGTGTGTCCTTCCTGTTAGAAGCCGCTGAAATCGCAAACACC 313

Db 184 GGTAAACGACGACGATCATCACCGTTCCATTAAAACGTAACCGCTAACGGCGTC 243

Db 314 GGAACGATGAAAGGATAATCATGATGATCATTAAGGAGGAAACACCCCTTC 373

QY 244 ACCAACGAGCTGGCTCAGAACAGCTGACCTGCGCTGATCTCTAG 303

Db 374 ACAATGCAAGGAGAGACATGATGATCATTAAGGAGGAAACACCCCTTC 433

QY 304 AAAAACCGCGGAAGAACTTCTGGAACTGAGCTAACGCTAACGCTAACGCTAAC 313

Db 434 AAAAACCGCGGAAGAACTTCTGGAACTGAGCTAACGCTAACGCTAACGCTAAC 493

QY 364 CAGCACCTGCTCTGTAACCGCTGCTGGAAAGATTCCTGA 405

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RESULT 15

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DEFINITION

ACCESSION CS045670

VERSION CS045670.1 GI: 61851968

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchoptolires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1. Abbas, A., Clark, H., Ouyang, W., Williams, P.M., Wood, W.I. and Wu, T.D.

AUTHORS

TITLE Compositions and methods for the treatment of immune related diseases

JOURNAL Patent: WO 2005019258 A 6224 03-MAR-2005; Genentech, Inc. (US)

FEATURES

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Title: US-10-735-149-27

Perfect score: 405

Sequence: 1 atgcgaatcgatcgcca.....acggttccgaaatccgtga 405

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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4: geneseqn201ab:\*

5: geneseqn201bs:\*

6: geneseqn202ab:\*

7: geneseqn202bs:\*

8: geneseqn203ab:\*

9: geneseqn203bs:\*

10: geneseqn200cs:\*

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13: geneseqn200bs:\*

14: geneseqn200s:\*

15: geneseqn200bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	405	100.0	405 12 ADP70484	ADP70484 Codon opt
2	299.6	74.0	483 6 AAS20695	Aas20695 Fragment
3	299.6	74.0	483 10 ADH4633	Adh4633 Human zal
4	299.6	74.0	483 10 ADI00969	Adi00969 Human zal
5	299.6	74.0	483 12 ADP792	Adp792 Human zal
6	299.6	74.0	483 14 ADW6416	Adw6416 Human zal
7	299.6	74.0	488 12 ADM41016	Adm41016 Human IL-
8	299.6	74.0	489 10 ADP17040	Adp17040 Human alb
9	299.6	74.0	489 14 ADP22801	Adp22801 Human psy
10	299.6	74.0	6 AAS75552	Aas75552 DNA encod
11	299.6	74.0	6 AAS20637	Aas20637 DNA encod
12	299.6	74.0	9 ADP4852	Adp4852 Human int
13	299.6	74.0	10 ADH4571	Adh4571 Human cdn
14	299.6	74.0	10 ADH0500	Adh0500 Immunity
15	299.6	74.0	12 ADP10556	Adp10556 Reference
16	299.6	74.0	12 ADP19730	Adp19730 Human zal
17	299.6	74.0	12 ADP70458	Adp70458 Human int
18	299.6	74.0		

**ALIGNMENTS**

Result No.	Score	Query Match Length	DB ID	Description
1	405	12 ADP70484	ADP70484 standard; cDNA; 405 BP.	
2	299.6	74.0	ADP70484;	
3	299.6	74.0	23-SEP-2004 (first entry)	
4	299.6	74.0	XX Codon optimised interleukin 21 (IL-21) encoding cDNA SEQ ID NO:27.	
5	299.6	74.0	XX interleukin 21; IL-21; human; gene; ss; codon optimised.	
6	299.6	74.0	XX Homo sapiens.	
7	299.6	74.0	OS Synthetic.	
8	299.6	74.0	XX	
9	299.6	74.0	PH Key	
10	299.6	74.0	FT CDS	
11	299.6	74.0	FT	
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WPI; 2004-500211/47.

P-PSDB; ADP70485.

**DR**

**XX**

**PR**

**PA**

**(ZYMO ) ZYMOGENETICS INC.**

**XX**

**PA**

**PI** Chang C, Zamost BL, Covert DC, Liu HY, De Jongh KS, Meyer JD; Holderman SD;

**XX**

**XX**

**WPI; 2004-500211/47.**

**P-PSDB; ADP70485.**

**DR**

**XX**

**PT** New expression vectors for the large-scale production of IL-21 proteins

**PT** comprises a prokaryotic origin of replication, a transcriptional initiation DNA element, a polymeric nucleotide sequence and a transcriptional terminator.



RESULT 3

ID44633 ADH44633 standard; DNA; 483 BP.

XX AC ADH44633;

XX DT 25-MAR-2004 (first entry)

DE Human zalphall ligand cDNA fragment.

XX KW Human; ss; zalphall ligand; zalphall receptor; immune response; tumour progression; metastasis; tumour stasis; hematopoietic tumour; lymphoma; B cell tumour; systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease; immunocompromised patient; HIV infection; vaccine; chromosome 4q27.

XX OS Homo sapiens.

XX PN US6605272-B2.

XX PD 12-AUG-2003.

XX PF 03-AUG-2001; 2001US-00923246.

XX PR 09-MAR-1999; 99US-0123547P.

PR 11-MAR-1999; 99US-0123904P.

PR 01-JUL-1999; 99US-0142013P.

PR 09-MAR-2000; 2000US-00522217.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

XX DR. WPI; 2003-895283/82.

XX PT Stimulating an immune response in a mammal exposed to an antigen or PT pathogen, useful for enhancing anti-tumor activity resulting in reduced tumor progression or metastasis, comprises administering zalphall ligand polypeptide.

XX PS Example 25; SEQ ID NO 63; 103pp; English.

CC The invention relates to stimulating an immune response in a mammal exposed to an antigen or pathogen comprises administering a composition comprising mature zalphall ligand polypeptide comprising residues 32-162 of ADH44632 in a pharmaceutical vehicle. Also included are stimulating an immune response in a mammal exposed to an antigen or pathogen (comprising: (a) determining (in)directly the level of antigen or pathogen present in the mammal; (b) administering a composition comprising zalphall ligand polypeptide in a pharmaceutical vehicle; (c) determining (in)directly the level of antigen or pathogen in the mammal; and (d) comparing the level of antigen or pathogen level in (a) with (b), where a change in the level indicates stimulation of immune response), and a pathogen (comprising: (a) determining a level of antigen or pathogen specific antibody; (b) administering a composition comprising zalphall ligand polypeptide in a pharmaceutical vehicle; (c) determining a post administration level of the antigen- or pathogen-specific antibody; and (d) comparing the level of the antibody in (a) with (b), where an increase in the antibody level indicates stimulation of immune response). The method is useful for stimulating an immune response in a mammal exposed to an antigen or pathogen, and for enhancing anti-tumour activity resulting in a reduction in tumour progression, decrease in metastasis, or tumour stasis. The tumour may be a haematopoietic tumour, a lymphoma or a B cell tumour. The zalphall ligand is useful for treating a wide range of diseases arising from defects in the immune system, e.g. systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or diabetes, for boosting immunity to infectious diseases, treating immunocompromised patients, such as HIV+ patients and in improving vaccines. The present sequence is a human Zalphall ligand cDNA (or

RESULT 4

AD100969 AD100969 standard; cDNA; 483 BP.

XX AC AD100969;

XX DT 22-APR-2004 (first entry)

DE Human zalphall ligand cDNA fragment - SEQ ID 63.

XX KW zalphall ligand; immunity; infectious disease; immunocompromised patient; HIV; vaccine; human; ss.

XX OS Homo sapiens.

XX PN US200312524-A1.

XX PD 03-JUL-2003.

XX PR 15-NOV-2002; 2002US-00295723.

XX PR 09-MAR-2000; 2000US-00522217.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

XX DR. WPI; 2003-811003/76.

XX PT New zalphall ligand polypeptides, useful for boosting immunity to infectious diseases, and treating immunocompromised patients, such as human immunodeficiency virus (HIV) patients, or in improving vaccines.

XX PS Example 25; SEQ ID NO 63; 113pp; English.

CC The invention relates to a novel isolated zaiaphall ligand polypeptide.  
CC The polypeptide of the invention may be useful for boosting immunity to  
CC infectious diseases and treating immunocompromised patients, such as HIV  
CC patients, as well as in improving vaccines. The current sequence is that  
CC of the human zaiaphall ligand cDNA fragment of the invention.  
XX  
SQ Sequence 483 BP; 167 A; 103 C; 96 G; 117 T; 0 U; 0 Other;

WPI; 2004-440401/41.  
New zalpha1I ligand  
treating cancer, e.g.  
lymphoma.

Query Match	74.0%	Score 299.6	DB 10	Length 483
Best Local Similarity	84.1%	Pred. No. 1.3e-83		
Matches	338	Conservative	0	Mismatches 64
Qy	4	CAAGCTGAGATGCCACATGATGAGAATGGCTCACTTAAGATATGTTGATAGCTG	63	
Db	82	CAAGGTCAGATGCCACATGATGAGAATGGCTCACTTAAGATATGTTGATAGCTG	141	
Qy	64	AAAATATTGTAATGACATGGTTCGGAAATTCTCTGGCCGGCTCGGAAGATGTTAGACC	123	
Db	142	AAAATATTGTAATGACATGGTTCGGCCGGCTCGGAAGATGTTAGACC	201	
Qy	124	AACTGTGACTGGTCCGTTCTCTGTTCCAGAAAGCCAGCTAAATCGCAACACC	183	
Db	202	AACTGTGACTGGTCCGTTCTCTGTTCCAGAAAGCCAACTAAAGTCAGCAATACA	261	
Qy	184	GGTGACAAAGAACATATCATCAACGTTCCATTAAAGAACTGAAAGTAAACCGCGTC	243	
Db	262	GGAACAACTGAAAGGATAATCAATGTTGATCAATTAAAGCTGAAAGGAAACCACTTC	321	
Qy	244	ACCAACGGCGGTCTCTGTCAGAAACCCGTCGACGCTGCCGCTCTGTGATTCCTATGAG	303	

The invention describes an isolated polypeptide comprising a sequence of amino acid residues that is at least 90 or 95% identical to residues 41 (Gln) to 148 (Ile), or 32 (Gln) to 148 (Ile) or a sequence of 162 amino acids (SEQ ID NO:2, human zalpha1b1 ligand), fully defined in the specification. Also described are: a pharmaceutical composition comprising the polypeptide, and a vehicle; a method of treating cancer in a mammal; a method of stimulating an immune response in a mammal with melanoma; a method of stimulating an immune response in a mammal bearing a tumour; an isolated polynucleotide comprising a sequence of nucleotides that encode amino acid residues cited above, where the polynucleotide encodes a polypeptide that binds a receptor comprising 538 amino acids, fully defined in the specification; a pharmaceutical composition comprising the polynucleotide encoding, in a pharmaceutically acceptable vehicle; an expression vector comprising the following operably linked elements: a control element; and a DNA segment comprising the polynucleotide; and an isolated polynucleotide molecule comprising at least 10 nucleotides of the polynucleotide sequence of 642 bp, fully defined in the specification. The molecules, compositions and methods are useful for treating cancer, e.g. melanoma, solid tumour, haematopoietic tumour, or lymphoma. This sequence represents a human zalpha1b1 ligand polynucleotide used in the creation of a zalpha1b1 ligand expression vector.

RESULT  
ADP19792  
ID ADP9792 standard: DNA: 483 BP.

Db	Dy	Sequence	Start	End
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142		AAAATATGAGTGAATGACTTGGTCCCGAAATTCTGGCACTCTGGAGAGATTTGAGACA	201	

Db	262	GGAACAAATGAAGGTTAATCAATGTCATTAAGCTGAAAGGGAAACCCCTCC	321
Qy	244	ACCAACGCGGGTGTCTTCAGAACCCGCTTGACCTGGCGCTGCTGATCTCTATGAG	303
Db	322	ACAAATGCGGAGAACAGAACAGACTAACATGCGCTTCATGTGATCTTGAG	381
Qy	304	AAAAAACCGCCGAGAAGATTCTGGAGCTTCAAATCCCTGCTGAGAAAATGATTCAC	363
Db	382	AAAACACCCAAAGATTTCTCTAGAAGATCTCAATCTCTCCAAAGATGATCTCAT	441
Qy	364	CAGCACCTGTCTCTGTACCCACGCTTCGGAGATCTCTGA	405
Db	442	CGCCATCTGCTCTAGAACACGAGAATGAGATTCCTGA	483

XX  
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;  
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;  
XX

XX  
XX  
AC  
XX  
DT 10-MAR-2005 (first entry)  
ADV96416;

DE	Human zalpha1 ligand cDNA sequence - SEQ ID 63.
XX	
KW	stem cell; cell culture; zalpha1 ligand; ss.
XX	
OS	Homo sapiens.
XX	
PN	US200420065-A1.
XX	
PD	23-DEC-2004.
XX	
PP	26-FEB-2004; 2004US-00707442.
XX	
PR	09-MAR-1999; 99US-0123547P.
PR	11-MAR-1999; 99US-0123904P.
PR	01-JUL-1999; 99US-0142013P.
PR	09-MAR-2000; 2000US-00522217.
XX	
PA	(NOVA/ ) NOVAK J E.
PA	(PRES/ ) PRESNELL S R.
PA	(SPRE/ ) SPRECHER C A.
PA	(POST/ ) FOSTER D C.
PA	(HOLD/ ) HOLLY R D.
PA	(GROS/ ) GROSS J A.
PA	(JOHN/ ) JOHNSTON J V.
PA	(NELS/ ) NELSON A J.
PA	(DILL/ ) DILLON S R.
PA	(HAMM/ ) HAMMOND A K.
XX	
PI	Novak JE, Presnelli SR, Sprecher CA, Foster DC, Holly RD; Gross JR, Johnston JV, Nelson AJ, Dillon SR, Hammond AK; DR WPI; 2005-036783/04.
XX	
PT	New zalpha 1I ligand fusion protein, useful for stimulating the proliferation and/or development of hematopoietic cells in vitro and in vivo, and in autologous marrow culture.
XX	
PS	Example 25; SEQ ID NO 63; 110pp; English.
CC	The invention comprises a fusion protein that contains a zalpha1 ligand and a cytokine polypeptide (e.g. IL-2, IL-4, IL-15 or GM-CSF), the fusion protein of the invention binds to the human receptor protein. The protein of the invention is useful for stimulating the proliferation and/or development of hematopoietic cells. The protein of the invention is also useful in autologous marrow culture. The present cDNA sequence represents a fragment of the human zalpha1 ligand coding sequence.
CC	
XX	
PS	Sequence 483 BP; 167 A; 103 C; 96 G; 117 T; 0 U; 0 Other;
CC	
CC	Query Match 74.0%; Score 299.6; DB 14; Length 483; Best Local Similarity 84.1%; Pred. No. 1.3e-83; Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
CC	
OY	4 CAAGCTCAAGATCGCCACATGATGATTGAGATGGTCACATTAGATGATTTGTTGATCGCTG 63
OY	82 CAAGCTCAAGATCGCCACATGATGATTGAGATGGTCACATTAGATGATTTGTTGATCGCTG 141
OY	64 AAAATTATGGTGAACCTGGTCCGGAAATCCGGCGCTCCGGAAAGGGTTGAGACC 123
OY	142 AAAATTATGGTGAACCTGGTCCGGAAAGGGTTGAGACC 201
DB	
OY	124 AACTCTGAGTGGTCCGCTTCTCCGTTCCAGAAAGCCACCTGAAATCCCAACACC 183
DB	202 AACGTTGAGGGTCTGTTCCGTTCTGAGGAGCCACTAAAGTCAGCAATACA 261
OY	184 GGTTACACAAACGAGCTATCATCAACGTTCCATTAAAGAACCTGAAACGTTAACC GGCGTCC 243
OY	262 GGAACACATGAGGAAATCATGATCAATTAAAGTCAGGAGAACCCCTTC 321
DB	244 ACCAAAGCAGGTCGCTGTCAGAAACCGTGTGACTGGCGCTGCTGATCTTGAG 303
OY	322 ACAATGTCAGGGAGAGACAGAACACAGACTAAAGCCCTCTGATGATCTTGAG 381
XX	
PS	Sequence 488 BP; 170 A; 103 C; 98 G; 117 T; 0 U; 0 Other;
CC	
CC	Query Match 74.0%; Score 299.6; DB 12; Length 488; Best Local Similarity 84.1%; Pred. No. 1.3e-83; Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
CC	
OY	4 CAAGCTCAAGATGGTCACATTAGATGATTTGATGAGCTG 63
DB	87 CAAGCTCAAGATGGTCACATTAGATGATTTGATGAGCTG 146
OY	64 AAAATTATGGTGAACCTGGTCCGGAAATCCGGCGCTCCGGAAAGGGTTGAGACC 123





QY	184	GGTACACAGGAACTTATCTAACTTCCATTAAAACCTGAAAGTAACCCGCTC	243	CC
CC	314	GGAAACATGAAAGATAATCACTATCAATTAAAGCTGAAAGTAACCCGCTC	243	CC
CC	244	ACCAAGCAGGCTGCTGCTGAGAAACCGCTGACTGCTGCCGCTCGTGTATGAG	303	CC
CC	374	ACAAATGAGGAGAGAACTGAAAGACAGACTAACTGCTGCTGTTATGAG	433	CC
Db	304	AAAAAACCCGAGAAAGATTCCTGAGAACCTGCTGAGAAATGTTCACTGAG	363	CC
QY	434	AAAAACACCAGAAATTCCTAGAAAGATTCAATCACTCTCCTCAAAAGATGATCAT	493	CC
QY	364	CAGCACCTGCTCTGACCTCCACGGTCCGAGTTCTGAG	405	CC
Db	494	CAGCTCTGCTCTAGAACACACCGAAGTCGAGTTCTGAG	535	CC
RESULT 11.				
ID	AAS20637	standard; cDNA; 642 BP.		
XX				
AC	AAS20637;			
XX				
DT	09-APR-2002	(first entry)		
XX				
DE	CDNA encoding human zalphall Ligand polypeptide.			
XX				
KW	Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor; natural killer cell proliferation; T-cell proliferation; B-cell proliferation; anti-tumour response; immune system; immunostimulant; cytostatic; human; gene therapy; hPBGS; activated human peripheral blood cell; ss.			
XX				
OS	Homo sapiens.			
FH	Location/Qualifiers			
FT	CDS			
FT	47. .535			
FT	/*tag= a			
FT	/product= "Zalphall Ligand"			
FT	47. .139			
FT	/*tag= b			
FT	140. .532			
FT	/*tag= c			
XX				
PN	US6307024-B1.			
XX				
PD	23-OCT-2001.			
XX				
PF	09-MAR-2000; 2000US-00522217.			
XX				
PR	09-MAR-1999; 99US-0123547P.			
PR	11-MAR-1999; 99US-0123904P.			
PR	01-JUL-1999; 99US-0142013P.			
XX				
PA	(ZYMO ) ZYMOGENETICS INC.			
XX				
PI	Novak JE, Presneill SR, Sprecher CA, Foster DC, Holly RD; Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK; DR			
XX				
DR	WPI; 2002-040208/05.			
XX				
PT	New zalphall ligand polypeptides and polynucleotides, useful for stimulating proliferation, activation, differentiation and/or induction of inhibition of specialized cell function, or for stimulating an antigenic response.			
XX				
PS	Example 7; Col 123-126; 105pp; English.			
XX				
CC	The present invention relates to the isolation of a novel cytokine, zalphall ligand and the polynucleotide encoding it. The invention also gives the sequence for the zalphall receptor and the polynucleotide encoding it. The zalphall Ligand polypeptide stimulates proliferation of			
CC	cells, proliferation of T-cells, proliferation of B-cells stimulated with anti-CD40 antibodies, stimulates an antigenic response in a mammal, and reduces proliferation of B-cells stimulated with anti-IGM antibodies. The zalphall Ligand polypeptide is also useful in preparing antibodies that bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can be used as probes or primers to clone regions of a zalphall Ligand gene, and in gene therapy. Zalphall Ligand may also be used to identify inhibitors of its activity, to enhance the generation of anti-tumour responses with or without the infusion of donor lymphocytes, and to activate or stimulate the immune system. The present sequence encoding from human zalphall Ligand polypeptide is isolated from a cDNA library from activated human peripheral blood cells (hPBGS).			
XX				
XX	Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;			
XX				
Query	Match	74.0%; Score 299.6; DB 6; Length 642;		
Matches	Best Local Similarity	84.1%; Pred. No. 1.5e-83;		
	Matches	338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;		
QY	4	CAAGGTCAGGTGCGCACATGATAGATGGTGTAGCTG	63	CC
Db	134	CAAGGTCAGGTGCGCACATGATAGATGGTGTAGCTG	193	CC
QY	64	AAAATTATGTAATGACCTGTTCCGGAAATCCGCCGCTCCGAA	123	CC
Db	194	AAAATTATGTAATGACTGTGCTGAAATTGCGCAACTAAGTCGAC	253	CC
QY	124	ACTGTGAGTGTGCGCTTCCCTGTTCCAGAAGGCCAGCTGAA	183	CC
Db	254	ACTGTGAGTGTGCTGTTCCGTTTCAGAAGGCCAGCTGAA	313	CC
QY	184	GTTAACACGAGCTGCTGCTGAACTTAAACCTGAAAGCTGAA	243	CC
Db	314	GGAAAGATGAAAGGATAATCAATGATCAATTAAAGCTGAA	373	CC
QY	244	ACCAAGGAGCTGCTGCTGAACTTAAACCTGAAAGCTGAA	243	CC
Db	374	ACAAATGCAAGGAGAACAGAACAGACTAACTGCTGCTG	433	CC
QY	304	AAAATCCGAGAAAGATTCCTGGAGCTTAATCCCTGCTGAGAA	363	CC
Db	434	AAAATCCGAGAAATTCCTAGAAAGATTCATCAACTCTCC	493	CC
QY	364	CAGCACCTGCTCTGCTGTAACCACTGGTTCCGAG	405	CC
Db	494	CAGCATCTGCTCTAGAACACGAGTCGAGATTCCTGAG	535	CC
RESULT 12.				
AAD47852				
ID	AAD47852	standard; DNA; 642 BP.		
XX				
AC	AAD47852;			
XX				
DT	27-AUG-2003	(first entry)		
XX				
XX	Human interleukin-21 (IL-21) DNA.			
KW	Interleukin-21; IL-21; antagonist; cancer; inflammatory; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; myasthenia gravis; diabetes; human; zalphall ligand; ds.			
KW	Homo sapiens.			
XX				
FH	Location/Qualifiers			
FT	CDS			
FT	47. .535			
FT	/*tag= a			
FT	/product= "IL-21"			
XX				
PN	WO2003040313-A2.			

PD 15-MAY-2003.

XX PF 28-OCT-2002; 2002WO-US034502.

XX PR 05-NOV-2001; 2001US-0337586P.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Presnell SR, West JW, Novak JE;

XX DR WPI; 2003-441547/41.

DR P-ESDB; AAE14932.

XX PT New IL-21 polypeptide and encoding polynucleotide, useful for diagnosing and treating disorders with aberrant expression or activity of the IL-21 polypeptide, such as cancer, rheumatoid arthritis, multiple sclerosis and diabetes.

XX PS Disclosure; Page 52-53; 71pp; English.

CC The invention relates to polynucleotides and polypeptides of interleukin-21 (IL-21) antagonists, that bind with specificity and exhibit an EC50 that is not detectable in receptor binding studies. The antagonists of the invention have mutations in the D helix of the IL-21 molecule, and can be used to inhibit the activity of IL-21 with its cognate receptor. The IL-21 antagonists are useful for diagnosing and treating disorders involving the aberrant expression or activity of the IL-21 polypeptide, such as cancer, inflammatory and autoimmune disorders, including rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, myasthenia gravis and diabetes. The polypeptides can also be used to prepare antibodies that bind IL-21 epitopes, peptides or polypeptides, and for enhancing in vitro killing of target tissues. The present sequence is human IL-21 (originally designated zalphall ligand) DNA.

XX SQ Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;

Query Match Best Local Similarity 74.0%; Score 299 6; DB 9; Length 642; Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0; Qy 4 CAAGCTCAAGTCGCCACATGATTAGAATGGTCACTATAGAATTTGATCAGCTG 63 CC 134 CAAGGTCAAGTCGCCACATGATTAGAATGGTCACTATAGAATTTGATCAGCTG 193 Qy 64 AAAATTATGTAATGACCTGTCGGAAATCCGGCGGCCCGAAAGGTGAGACC 123 Db 194 AAAATTATGTAATGACCTGTCGGAAATCCGGCGGCCCGAAAGGTGAGACC 253 Qy 124 ACTGTGAGTGTCGCTTCCTCCCTGTTCCAGAAAGGCCAGCTGAATCCGAAACCC 183 Db 254 ACTGTGAGTGTCGCTTCCTCCCTGTTCCAGAAAGGCCAGCTGAATCCGAAATCA 313 Qy 184 GGTAAACAAACGACGATCATCAACCTTCCATTAAAGAACGTAAACCGCGTCC 243 Db 314 GGAACACAACTGAAAGATAATCCATGATTTAAAGGTGAGAGAACCCCTCC 373 Qy 244 ACCAACGCGGTCGTCAGAACACCGCTGACCTGCGCCGCTGTGATCTTATGAG 303 Db 374 ACAATGCGAGGAGAGACGAAACGACGACTAACATGCCCTCATGTGATCTTATGAG 433 Qy 304 AAAAACCGCGAAAGAATTCCTGCAAAATCCGCTGAGAAATGATTCA 363 Db 434 AAAAACCGCCAAAGAACATTCCTGAGAAAGATTCATCACTCTCCAAAGATGATCAT 493 Qy 364 CAGCACCTGCTCTGTCGACCCACGGTCCGAGAAATTCCTG 405 Db 494 CAGCATCTGCTCTGAGAACACCGAAGTGAAGATTCCTG 535

AC ADH44571;

XX 25-MAR-2004 (first entry)

XX DT Human cDNA encoding Zalphall ligand.

XX KW Human; ss; Zalphall ligand; Zalphall receptor; immune response; tumour progression; metastasis; tumour stasis; haematopoietic tumour; lymphoma; B cell tumour; Systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis; diabetes; infectious disease; immunocompromised patient; HIV infection; vaccine; chromosome 4q27.

XX OS Homo sapiens.

XX PN US6605272-B2.

XX PD 12-AUG-2003.

XX FP 03-AUG-2001; 2001US-00932346.

XX PR 09-MAR-1999; 99US-0123547P.

XX PR 11-MAR-1999; 99US-0123904P.

XX PR 01-JUL-1999; 99US-0142013P.

XX PR 09-MAR-2000; 2000US-00522217.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD, Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK; DR WPI; 2003-895283/82.

XX PT Stimulating an immune response in a mammal exposed to an antigen or pathogen, useful for enhancing anti-tumour activity resulting in reduced tumor progression or metastasis, comprises administering zalphall ligand polypeptide.

XX PS Example 7; SEQ ID NO 1; 103pp; English.

CC The invention relates to stimulating an immune response in a mammal exposed to an antigen or pathogen comprises administering a composition comprising mature Zalphall ligand polypeptide comprising residues 32-162 of ADH44572 in a pharmaceutical vehicle. Also included are stimulating an immune response in a mammal exposed to an antigen or pathogen (comprising: (a) determining (indirectly) the level of antigen or pathogen present in the mammal; (b) administering a composition comprising zalphall ligand polypeptide in a pharmaceutical vehicle; (c) determining (indirectly) the level of antigen or pathogen in the mammal; and (d) comparing the antigen or pathogen level in (a) with (b), where a change in the level indicates stimulation of immune response) and stimulating an immune response in a mammal exposed to an antigen or pathogen (comprising: (a) determining a level of antigen- or pathogen-specific antibody; (b) administering a composition comprising zalphall ligand polypeptide in a pharmaceutical vehicle; (c) determining a post administration level of the antigen- or pathogen-specific antibody; and (d) comparing the level of the antibody in (a) with (b), where an increase in the antibody level indicates stimulation of immune response). The method is useful for stimulating an immune response in a mammal exposed to an antigen or pathogen, and for enhancing anti-tumour activity resulting in a reduction in tumour progression, decrease in metastasis, or tumour stasis. The tumour may be a haemopoietic tumour, a lymphoma, or a B cell tumour. The zalphall ligand is useful for treating a wide range of diseases arising from defects in the immune system, e.g. systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, or diabetes, for boosting immunity to infectious diseases, treating immunocompromised patients, such as HIV patients and in improving vaccines. The present sequence is a human Zalphall ligand cDNA (or fragment).

XX SQ Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;

XX Query Match Best Local Similarity 74.1%; Pred. No. 1.5e-83;

XX ID ADH44571; ADH44571 standard; cDNA; 642 BP.

RESULT 13

Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGGTCAGATGCCACATGATTAGATGCGTCAACTATAGATATGTTGATCAGTG 63  
 Db 134 CAAAGGTCAGATGCCACATGATTAGATGCGTCAACTATAGATATGTTGATCAGTG 193

Qy 64 AAAATTATGTTGAAATGACCTGTTCCGGATTCCTGGCGCTCCGGAGATGTTGAGACC 123  
 Db 194 AAAATTATGTTGAAATGACCTGTTCCGGATTCCTGGCGCTCCGGAGATGTTGAGACC 253

Qy 124 AACCTGTGAGTGTGTCGCTTCTCTGTTCCAGAAAGCCAGCTGAATCCGAAACACC 183  
 Db 254 AACCTGTGAGTGTGTCGCTTCTCTGTTCCAGAAAGCCAGCTGAATCCGAAACACC 313

Qy 184 GGTAAACAAAGAAAGTCACTCAAGCTTCCATTAAGAAACTGAAACGTAACCGCCGCC 243  
 Db 314 GGTAAACAAAGAAAGTCACTCAAGCTTCCATTAAGAAACTGAAACGTAACCGCCGCC 373

Qy 304 AAAAACCGCCGAAAGAAATTCCTGAAACCTTCAATCCTGTCGAGAAATGATCAC 363  
 Db 434 AAAAACCGCCGAAAGAAATTCCTGAAACCTTCAATCCTGTCGAGAAATGATCAC 493

Qy 364 CAGCACCGTCCTCGTCTGACCGGTCGAGGATTCCTGA 405  
 Db 494 CAGCACCGTCCTCGTCTGACCGGTCGAGGATTCCTGA 535

RESULT 14

AD100907 ID AD100907 standard; cDNA; 642 BP.

AC AD100907;

XX DT 22-APR-2004 (first entry)

DE Immunity-related human zalphall ligand cDNA.

XX KW zalphall ligand; immunity; infectious disease; immunocompromised patient; HIV; vaccine; human; ss; gene.

OS Homo sapiens.

US2003125524-A1.

PN 03-JUL-2003.

PF 15-NOV-2002; 2002US-00295723.

PR 09-MAR-2000; 2000US-0052217.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PT Novak JB, Presnell SR, Sprecher CA, Foster DC, Holly RD; Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK; WBT; 2003-811003/76.

DR P-PSDB; AD100908.

XX PT New zalphall ligand polypeptides, useful for boosting immunity to infectious diseases, and treating immunocompromised patients, such as human immunodeficiency virus (HIV) patients, or in improving vaccines.

PS Claim 19; SEQ ID NO 1; 113pp; English.

CC The invention relates to a novel isolated zalphall ligand polypeptide.

CC The polypeptide of the invention may be useful for boosting immunity to infectious diseases and treating immunocompromised patients, such as HIV patients, as well as in improving vaccines. The current sequence is that of the human zalphall ligand cDNA of the invention.

XX SQ Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;

Query Match 74.0%; Score 299.6; DB 10; Length 642; Best Local Similarity 84.1%; Pred. No. 1.5e-83; Mismatches 64; Indels 0; Gaps 0;

Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGGTCAGATGCCACATGATTAGATGCGTCAACTATAGATATGTTGATCAGTG 63  
 Db 134 CAAAGGTCAGATGCCACATGATTAGATGCGTCAACTATAGATATGTTGATCAGTG 193

Qy 64 AAAATTATGTTGAAATGACCTGTTCCGGATTCCTGGCGCTCCGGAGATGTTGAGACC 123  
 Db 194 AAAATTATGTTGAAATGACCTGTTCCGGATTCCTGGCGCTCCGGAGATGTTGAGACC 253

Qy 124 AACCTGTGAGTGTGTCGCTTCTCTGTTCCAGAAAGCCAGCTGAATCCGAAACACC 183  
 Db 254 AACCTGTGAGTGTGTCGCTTCTCTGTTCCAGAAAGCCAGCTGAATCCGAAACACC 313

Qy 244 ACCACACGGGTCCTGTCAGAACACCCCTGACCTGCCGCTCTGATCTTATAG 303  
 Db 374 ACCACACGGGTCCTGTCAGAACACCCCTGACCTGCCGCTCTGATCTTATAG 433

Qy 304 AAAAACCGCCGAAAGAAATTCCTGAAACCTTCAATCCTGTCGAGAAATGATCAC 363  
 Db 434 AAAAACCGCCGAAAGAAATTCCTGAAACCTTCAATCCTGTCGAGAAATGATCAC 493

Qy 364 CAGCACCGTCCTCGTCTGACCGGTCGAGGATTCCTGA 405  
 Db 494 CAGCACCGTCCTCGTCTGACCGGTCGAGGATTCCTGA 535

RESULT 15

AD10500 ID AD10500 standard; DNA; 642 BP.

XX AC ADH10500;

XX DT 11-MAR-2004 (first entry)

DE Human interleukin-21 (IL-21) encoding DNA.

XX KW II-21; interleukin-21; cytostatic; virucide; antiinflammatory; hepatotropic; neuroprotective; muscular; respiratory; antiarthritic; antibacterial; anti-HIV; gene therapy; cancer; human; gene; ds.

OS Homo sapiens.

XX FH Key FT CDS Location/Qualifiers 47..535  
 FT /\*tag= a /product= "interleukin-21"  
 FT WO2003103589-A2.

XX PD 18-DEC-2003.

XX PF 06-JUN-2003; 2003WO-US017808.

XX PR 07-JUN-2002; 2002US-038712P.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Nelson AJ, Hughes SD, Holly RD, Kindsvogel WR;

XX DR WPT; 2004-062206-06.

XX PR P-PSDB; ADH10501.

XX PT Treating Non-Hodgkin's lymphoma, cancer or infection comprises

PT administering to the subject a polypeptide having a functional activity

PT

of interleukin-21.

XX

PS Disclosure; SEQ ID NO 1; 154pp; English.

The invention relates to treating Non-Hodgkin's lymphoma, cancer or infection and involves administering to the subject a polypeptide having a functional activity of interleukin-21 (IL-21). The methods are useful for treating Non-Hodgkin's lymphoma; cancer such as renal cell carcinoma, epithelial carcinoma, breast cancer, prostate cancer, ovarian cancer and colon cancer; viral infection such as AIDS, Hepatitis B or C virus, gastroenteritis, haemorrhagic diseases, enteritis, carditis, encephalitis, paralytic, bronchitis, upper or lower respiratory disease, meningitis, and mononucleosis; or bacterial infection, such as an infection by a bacterium selected from chlamydiae, listeriae, helicobacter pylori, mycobacterium, mycoplasma, salmonella, and shigella, or sudden acute respiratory syndrome caused by a coronavirus, Herpes Simplex viruses, Epstein-Barr virus, Cytomegalovirus, Papilloma virus, Adenovirus, Poliovirus, Orthomyxoviruses, Paramyxoviruses, influenza viruses, caliciviruses, rabies viruses, and rinderpest viruses. The present sequence represents a DNA encoding a human IL-21 polypeptide.

SQ Sequence 642 BP; 220 A; 127 C; 129 G; 166 T; 0 U; 0 Other;

Query Match 74.0%; Score 299.6; DB 12; Length 642;

Best Local Similarity 84.1%; Pred. No. 1.5e-83; Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy	4	CGAGCTCAAGTCGCCACATGATTAGATGCTCACTTATAGATTTGATGACCTG	63
Db	134	CGAGGTCAAGATGCCACATGATTAGATGCTCACTTATAGATTTGATGACCTG	193
Qy	64	AAAATTATGTTGATGACTGCTGTCGGAAATTCCTCGGGCTGAAATCGGAAACACC	123
Db	194	AAAATTATGTTGATGACTGCTGTCGGAAATTCCTCGGGCTGAAATCGGAAACACC	253
Qy	124	ACTGTGAGTGTCCCTTTCCTGTTCCAGAAGGCCCGCTGAAATCGGAAACACC	183
Db	254	ACTGTGAGTGTCCCTTTCCTGTTCCAGAAGGCCCGCTGAAATCGGAAACACC	313
Qy	184	GTGTACGACGACGTTACATGTTCCATTAAAGCTGAAGGTAACGGGTCC	243
Db	314	GGAAACAAATGAAGAATAATGATGATCAATTAAAGCTGAAGGGAAACCTTCC	373
Qy	244	ACCAAGCGAGCGTGTGTCAACACCGCTGACCTGGCCGCTCCTGTGATCTPATGAG	303
Db	374	ACCAAGCGAGCGAGACGACGACGTTACATGCTTCTATGTGATCTPATGAG	433
Qy	304	AAAACACCGGGAAAGAATTCTGGAGCTTCATAATCCCTGGAGAAATGATTAC	363
Db	434	AAAACACCGGGAAAGAATTCTTAGAGATCATCTCTCCAAAGATGATTAC	493
Qy	364	CAGCACCTGCTCTGTTACCGCTCCGGTCAAGATTCTCGA	405
Db	494	CAGCACCTGCTCTGTTACCGCTCCGGTCAAGATTCTCGA	535

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Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.9					
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C	299.6	74.0	582	5	CD559457	
C	299.6	74.0	582	5	CD559461	
C	299.6	74.0	583	5	CD559456	
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C	299.6	74.0	592	5	CD559614	
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C	298	73.6	600	5	CD559613	
C	296.4	73.2	581	5	CD559460	
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c	25	67.2	16.6	539	12	BZ937073
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c	33	57.6	14.2	365	4	BY220565
c	34	57.4	14.2	812	2	BI51560
c	35	50	12.3	584	13	C2026087
c	36	46.4	11.5	880	14	CT053999
c	37	40.4	10.0	101	11	AZ435999
c	38	40.2	9.9	358	4	BY213229
c	39	38.8	9.6	1302	12	BY2572734
c	40	37.8	9.3	647	11	BH013521
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Query Match 74.0%; Score 299.6; DB 14; Length 489;  
 Best Local Similarity 84.1%; Pred. No. 9.5e-83; Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAAGTCAGATGCCACATGATTAGATGGCTGCAACTATAGATATGTTGATCAGTC 63  
 Db 88 CAAAGTCAGATGCCACATGATTAGATGGCTGCAACTATAGATATGTTGATCAGTC 147

Qy 64 AAAATTATGTTGACTGCTGGTCCGAAATCTGCGGAGATGTGAGGCC 123  
 Db 148 AAAATTATGTTGACTGCTGGTCCGAAATCTGCGGAGATGTGAGGCC 207

Qy 124 ACTGTGAGTGTGTCGCCCTCTCTGTTCCAGAAAGCCAGCTGAATCCGCAACCC 183  
 Db 208 ACTGTGAGTGTGTCGCCCTCTGTTCCAGAAAGCCAGCTGAATCCGCAACCC 267

Qy 184 GTCACAAAGAACCTATCATCACTAACGTTCAATAAAACCTAAACGTAACCGCCGTC 243  
 Db 268 GAAACATGAAAGATAATCTATGTCATTAACAGCTGAGAGGAAACCTTC 327

Qy 244 ACCAACGAGGTGTCGTCAGAACACGGTCACCTGCCGCTGATTTATGAC 303  
 Db 328 ACAAATGAGGAGAACAGAACAGAACAGACTAACATGCGCTCATGATCTATGAC 387

Qy 304 AAAAACCCCGAAAGAACATCTCGGAAGCTTCAATCCCTGTCGAGAAATGATTAC 363  
 Db 388 AAAAACCCCAAGAACATCTCCAAAGATCTGAGAAAGATCAATCTCCAAAGATGATTAC 447

Qy 364 CAGCACCTGTCCTCGTACCCACGGTTCGGAGATTCTGA 405  
 Db 448 CAGCATCTCTAGACACACGGAACTGAGATTCTGA 489

RESULT 2  
 CD559455/c

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 IMAGE:6971867 3', mRNA sequence.

ACCESSION CD559455  
 VERSION CD559455.1  
 KEYWORDS EST.  
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 ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 566)  
 AUTHORS NIH\_MGC http://mgc.ncbi.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Daniela S. Gerhard, Ph.D.  
 National Cancer Genomics Office of Cancer Genomics National Cancer Institute / NIH  
 Bldg. 31 Rm1047 Bethesda, MD 20892  
 Email: cgabs@mail.nih.gov  
 Tissue Procurement: Narayan Bhat  
 CDNA Library Preparation: Bhat Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINTL at:  
 http://image.lnl.gov  
 http://image.lnl.gov  
 High quality sequence stop: 566.

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 /clone\_lib="NIH\_MGC\_195"

RESULT 3  
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DEFINITION CD559609 573 bp mRNA linear EST 26-Nov-2003  
 AGENCOURT 14496932 NIH\_MGC\_195 Homo sapiens cDNA clone  
 IMAGE:6971866 5', mRNA sequence.

ACCESSION CD559609  
 VERSION CD559609.2  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 573)  
 AUTHORS NIH\_MGC http://mgc.ncbi.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT On Jun 10 2003 this sequence version replaced g1:31585677.  
 Contact: Daniela S. Gerhard, Ph.D.  
 National Cancer Institute / NIH

/note="Vector: PDNR-Dual; Site\_1: loxP-Sall; Site\_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cDNA (from 30 cell lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bern III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at: ftp://image.lnl.gov/image/rearrayed\_plates/IRBK.preSV.dat a Note: this is a NIH MGC Library."

Query Match 74.0%; Score 299.6; DB 5; Length 566;  
 Best Local Similarity 84.1%; Pred. No. 9.5e-83; Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGTCAGATGCCACATGATTAGATGGCTGCAACTATAGATATGTTGATCAGTC 63  
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Qy 64 AAAATTATGTTGACTGCTGGTCCGGAAATCTGCGGCTCCGGAGATCTGAGACC 123  
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Qy 124 ACTGTGAGTGTGTCGCCCTCTGTTCCAGAAAGCCAGCTGAATCCGCAACCC 183  
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Qy 184 GTCACAAAGAACCTATCATCACTAACGTTCAATAAAACCTAAACGTAACCGCCGTC 243  
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Qy 244 ACCAACGAGGTGTCGTCAGAACACGGTCGACCTGCCGTCCTGATCTTATGAC 303  
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Qy 364 CAGCACCTGTCCTCGTACCCACGGTTCGGAGATCTCTGA 405  
 Db 73 CAGCATCTCTAGACACACGGAACTGAGATTCTGA 32

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgbabs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC Clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Plate: IRBK2 row: 9 column: 09

High quality sequence start: 573.

## FEATURES SOURCE

### Location/Qualifiers

1. . 573  
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 PCR-amplified using gene-specific primers to contain the  
 complete open reading frame (based on known gene sequences  
 available from NCBI's RefSeq). Template for PCR is cDNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/Clontech and Washington University).  
 PCR products are directionally cloned into the loxp sites  
 of the PDR-Dual vector. Library constructed by Dr.  
 Narayan Bhat, Earl Bore III and Hongling Liao (Gene  
 Expression Laboratory, Research Technology Program, SAIC  
 Frederick, NCI-Frederick, Frederick, MD 21702). For  
 information on which gene each clone represents, please  
 visit our anonymous ftp site at  
 ftp://image.llnl.gov/image/rearranged\_plates/IRBK.presv.dat  
 a Note: this is a NIH\_MGC library."

## ORIGIN

Query Match 74.0%; Score 299.6; DB 5; Length 573;

Best Local Similarity 84.1%; Pred. No. 9.9e-83; Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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QY 124 ACTGTGAGTGTGCTGTTCCCGTTCCGAAAGGCCAGCTGAATCCGCACACC 183

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 Db 319 GAAACAACTGAAAGGATATCAATGTATCAATTAAAGCTGAGAGGAAACCTTC 378

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Query Match 74.0%; Score 299.6; DB 5; Length 581;

Best Local Similarity 84.1%; Pred. No. 9.9e-83; Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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Db 439 AAAACACCACCAAGAATCTGAGATCTCAATCTCCAAAGATCT 498

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CD559459/C LOCUS CD559459 DEFINITION AGENCOURT 14496771 NIH\_MGC\_195 Homo sapiens cDNA clone IMAGE:6971863 5', mRNA sequence. ACCESSION CD559459 VERSION CD559459.2 GI:3845485 KEYWORDS EST. SOURCE Homo sapiens (human)  
 Homo sapiens  
 Birkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo  
 1 (bases 1 to 581)  
 NIH-MGC http://mgc.nci.nih.gov/  
 AUTHORS National Cancer Institute / NIH  
 TITLE Unpublished (1999)  
 JOURNAL On Jun 10, 2003 this sequence version replaced gi:31585527.  
 COMMENT Contact: Daniel S. Gerhard, Ph.D.  
 Tissue Procurement: Narayan Bhat  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgbabs-r@mail.nih.gov  
 Tissue Procurement: Bhat Laboratory  
 CDNA Library Preparation: Bhat Laboratory  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov/  
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 High quality sequence start: 21  
 Location/Qualifiers

## FEATURES SOURCE

### Location/Qualifiers

1. . 581  
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 /note="Vector: PDR-Dual; Site\_1: loxP-SalI, Site\_2:  
 loxP-HindIII; Clones from this library have been  
 PCR-amplified using gene-specific primers to contain the  
 complete open reading frame (based on known gene sequences  
 available from NCBI's RefSeq). Template for PCR is cDNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/Clontech and Washington University).  
 PCR products are directionally cloned into the loxp sites  
 of the PDR-Dual vector. Library constructed by Dr.  
 Narayan Bhat, Earl Bore III and Hongling Liao (Gene  
 Expression Laboratory, Research Technology Program, SAIC  
 Frederick, NCI-Frederick, Frederick, MD 21702). For  
 information on which gene each clone represents, please  
 visit our anonymous ftp site at  
 ftp://image.llnl.gov/image/rearranged\_plates/IRBK.presv.dat  
 a Note: this is a NIH\_MGC library."

## ORIGIN

Query Match 74.0%; Score 299.6; DB 5; Length 581;

Best Local Similarity 84.1%; Pred. No. 9.9e-83; Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 4 CAAGCTCAAGATCSCCACATGATAGAATGGTCACTATAGATATGTTGAGCTG 63  
 Db 448 CAAGCTCAAGATCSCCACATGATAGAATGGTCACTATAGATATGTTGAGCTG 389

QY 64 AAAATTAGTGTAGTGTGACTGTTCCGAGAATTCCTGCGGCTCGGAGATGTGAGCC 123  
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FEATURES	High quality sequence stop: 582.	REFERENCE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
Source	Location/Qualifiers	AUTHORS	1. (bases 1 to 583)
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	/organism="Homo sapiens"	JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
	/mol_type="mRNA"	COMMENT	Unpublished (1998)
	/db_xref="taxon:9606"		On Jun 10, 2003 this sequence version replaced gi:31585524.
	/clone="IMAGE:6971861"	CONTACT	Contact: Daniela S. Gerhard, Ph.D.
	/lab_host="DH5A (T1 phage-resistant)"		Office of Cancer Genomics
	/clone lib="DH5A (T1 phage-resistant)"		National Cancer Institute / NIH
	/note="vector: PDR-Dual; Site_1: loxp-Sall; Site_2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the pDNR-dual vector. Library constructed by Dr. Narayan Bhat, Earl Bore III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat		Bldg. 31 Rm10A07 Bethesda, MD 20892
	a Note: this is a NIH_MGC Library."		Email: cagpob@mail.nih.gov
ORIGIN			Tissue Procurement: Narayan Bhat
	Query Match 74.0%; Score 299.6; DB 5; Length 582; Best Local Similarity 84.1%; Pred. No. 9.9e-83; Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;		cDNA Library Preparation: Bhat Laboratory
	4 CAAGGTCAAGTCGCCACATGATTAGATGGTCACATAGATGTTGATCAGTC 63		CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	449 CAAGGTCAAGTCGCCACATGATTAGATGGTCACATAGATGTTGATCAGTC 390		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
	64 AAAATTATGTAATGACTGTTCCGANTTCCTCGCGCTCCGGAGAGTGTGAGAC 123		Plate: IRBK2 row: 9 column: 09
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	269 GGAACAAATGAAAGGATAATGATGATCAATTAAAGCTGAAGGAGAACCTTC 210		/mol_type="mRNA"
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	89 CAGCATCTGTCCTCTGAAACACAGGAAGTTCCTGA 48		
ORIGIN			
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 Db 150 AAGGACCCAGATCTCTGAGATCTCACTTCCAGAGATGATTCA 91

Qy 364 CAGCACCTGTCCTCTGACCCAGGTCGGAGATTCTGA 405  
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RESULT 8  
 LOCUS CD559612 583 bp mRNA linear EST 26-NOV-2003  
 DEFINITION AGENCOURT 14496744 NIH\_MGC 195 Homo sapiens cDNA clone  
 IMAGE:6971863 5', mRNA sequence.

ACCESSION CD559612  
 VERSION CD559612.2 GI:38558948

KEYWORD SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchoptoglires; Primates; Catarrhini; Hominidae; Homo.

TITLE JOURNAL Unpublished (1999)

COMMENT On Jun 10, 2003 this sequence version replaced gi:31585680.  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapbs-@email.nih.gov

Tissue Procurement: Narayan Bhat  
 cDNA Library Preparation: Bhat Laboratory  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:  
<http://image.llnl.gov>

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FEATURES source

1. .583  
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[ftp://image.llnl.gov/image/rearranged\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat)  
 a Note: this is a NIH\_MGC library."

ORIGIN

Qy 4 CAAGGTCAAGATGCCAACATGATTAGAATGCGTCAACTTATAGATATTGTGATCAGTG 63  
 Db 151 CAAGGTCAAGATGCCAACATGATTAGAATGCGTCAACTTATAGATATTGTGATCAGTG 210

Qy 64 AAAATTATGTTGATGACTGTGTTCCGAGATGTTGAGGCC 123  
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Qy 124 AACGTGGTGGCGCTTCCTCTGTTCCAGAAAGCCACGTGAAATCCGAAACCC 183  
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Qy 184 GGTAACACAGAACCTATCACTAACGTTCCATTAAMAAACTGAAACGTAAACGGCGTCC 243  
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Qy 304 AAAAACCCGAGAGATTCCTGAGACAGACTACATGCCCTCATGTTGATTAG 363  
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RESULT 9  
 LOCUS CD559614 592 bp mRNA linear EST 26-NOV-2003  
 DEFINITION AGENCOURT 14496629 NIH\_MGC\_195 Homo sapiens cDNA clone  
 IMAGE:6971861 5', mRNA sequence.

ACCESSION CD559614  
 VERSION CD559614.2 GI:38559591

KEYWORD SOURCE Homo sapiens (human)  
 ORGANISM Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchoptoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/  
 TITLE JOURNAL Unpublished (1999)  
 COMMENT On Jun 10, 2003 this sequence version replaced gi:31585680.  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapbs-@email.nih.gov

Tissue Procurement: Narayan Bhat  
 cDNA Library Preparation: Bhat Laboratory  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:  
<http://image.llnl.gov>

Plate: IRBK2 row: g column: 04  
 High quality sequence stop: 592.

FEATURES source

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Query Match 74.0%; Score 299.6; DB 5; Length 583;  
 Best Local Similarity 84.1%; Pred. No. 9.9e-83;  
 Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the PDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bore III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [ftp://image.llnl.gov/image/rearranged\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat)

## ORIGIN

Query Match 74.0%; Score 299.6; DB 5; Length 592;  
Best Local Similarity 84.1%; Pred. No. 1e-82; Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGGTCAAGTCGCCACATGATAGAATGGTCACTTAAGATATTGTGATCAGCTG 63  
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Qy 64 AAAATTATGTAATGGACTCTGGTCCGGAAATTCCTCGCCGCGCTCCGGAAAGATGTGAGACC 123  
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Qy 124 AACTGTGAGTGTCGCTTCTCCGTTCCAGAAGACCCACCTGAATGCCAACACC 183  
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Db 338 GGAAACACATGAAAGATTAATCATCTTCAATTAAGCTGAAAGGAAACCCACCTCC 397  
Qy 244 ACCAACGCGGTCTGTCGTCAGAACACCGCTGTGACTGCCGCTGTGATCTGTAG 303  
Db 398 ACAATTGCAAGGAGAGACAGAACACAGACTAACATGCGCTTCAGTGATCTGTAG 457  
Qy 304 AAAAACCGCGGAAGAACCTCTGGACGTTCAATCCCTCCAGAAAGATATTGAC 363  
Db 458 AAAAACACCAACCCAAAGAACATTCTAGAAAGATCAATCACTCTCCAAAGATGATTCA 517  
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## ORIGIN

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Best Local Similarity 84.1%; Pred. No. 1e-82; Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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Db 285 AACTGTGAGTGTCGCTTCTCCGTTCCAGAAGGCCCACCTGAATGCCAACACC 344  
Qy 184 GGTTACACACGACGATCATCAACGGTTCCTGAAACACCGCTGTGACTGCCGCGTCC 243  
Db 345 GGAAACACATGAAAGATTAATCATCTTCAATTAAGCTGAAAGGAAACCCACCTTC 404  
Qy 244 ACCAACGCGGTCTGTCGTCAGAACACCGCTGTGACTGCCGCGTCC 303  
Db 405 ACAATTGCAAGGAGAGACAGAACACGACTAACATGCGCTTCAGTGATCTGTAG 464  
Qy 304 AAAAACCGCGGAAGAACCTCTGGACGTTCAATCCCTGTCAGAAAGATATTGAC 363  
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## Tissue Procurement: Narayan Bhat

cDNA Library Preparation: Bhat Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNU)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNU at: <http://image.llnl.gov>

Plate: IRBK2 row: 9 column: 08

High quality sequence start: 13

High quality sequence stop: 599.

## FEATURES

## SOURCE

1..599  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone=IMAGE:6971865"

/tissue type="mixed"  
/lab\_host="IRBK (TL phage-resistant)"  
/clone.lib="NIH\_MGC\_135"  
/note="vector: PDNR-Dual; Site 1: loxp-SAI1; Site 2: loxp-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI, RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxp sites of the PDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bore III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at [ftp://image.llnl.gov/image/rearranged\\_plates/IRBK.presv.dat](ftp://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat)

a Note: this is a NIH\_MGC Library.

RESULT 11

CD559613

Query Match 74.0%; Score 299.6; DB 5; Length 599;  
Best Local Similarity 84.1%; Pred. No. 1e-82; Matches 338; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 4 CAAGGTCAAGTCGCCACATGATAGAATGGTCACTTAAGATATTGTGATCAGCTG 63  
Db 165 CAAGGTCAAGTCGCCACATGATAGAATGGTCACTTAAGATATTGTGATCAGCTG 224  
Qy 64 AAAATTATGTAATGGACTCTGGTCCGGAAATTCCTCGCCGCGCTCCGGAAAGATGTGAGACC 123  
Db 225 AAAATTATGTAATGGACTCTGGTCCGGAAATTCCTCGCCGCGCTCCGGAAAGATGTGAGACA 284  
Qy 124 AACTGTGAGTGTCGCTTCTCCGTTCCAGAAGACCCACCTGAATGCCAACACC 183  
Db 285 AACTGTGAGTGTCGCTTCTCCGTTCCAGAAGGCCCACCTGAATGCCAACACC 344  
Qy 184 GGTTACACACGACGATCATCAACGGTTCCTGAAACACCGCTGTGACTGCCGCGTCC 243  
Db 345 GGAAACACATGAAAGATTAATCATCTTCAATTAAGCTGAAAGGAAACCCACCTTC 404  
Qy 244 ACCAACGCGGTCTGTCGTCAGAACACCGCTGTGACTGCCGCGTCC 303  
Db 405 ACAATTGCAAGGAGAGACAGAACACGACTAACATGCGCTTCAGTGATCTGTAG 464  
Qy 304 AAAAACCGCGGAAGAACCTCTGGACGTTCAATCCCTGTCAGAAAGATATTGAC 363  
Db 465 AAAAACACCAACCCAAAGAACATTCTAGAAAGATCAATCACTTCTCCAAAGATGATTCA 524  
Qy 364 CAGCACCTGTCCTCTGGTCCGGAAAGTTCCTGA 405  
Db 525 CAGCATCTGCTCTAGAACACCGAGTGAAGTTCCTGA 566

RESULT 11

CD559613

LOCUS	CD559613	600 bp mRNA linear EST 26-NOV-2003	Db	286	AACTGTGAGTGGTCAGCTTTCCTGCCTTCAGAAGGCCAACTAAGTCAGCAATCA 345
DEFINITION	AGENCOURT 14496682 NIH_MGC_195 Homo sapiens cDNA clone		Qy	184	GCTAACACAGAACGTTATCAACGTTCCATTAACACTGAAACGTAACGCCGCC 243
ACCESSION	IMAGE:6971862 5', mRNA sequence.		Db	346	GGAAACAATGAAAGGATAATCAATGATCAATTAAAGCTGAGAGAAACACCTTC 405
VERSION	CD559613		Qy	244	ACCAACGCGGTCCTCGTCAGAACACCGCTGACTCCGTCCTGAGATCTTATG 303
KEYWORDS	EST		Db	405	ACAAATGAGGGAGAACGAGAACAGACAGACTACATGCCCTCATGATGATCTATG 465
REFERENCE	Homo sapiens (human)		Qy	304	AAAAAACCGCGAAAGAAATTCTCGAAGCTTCATAATCCCTGCTGAGAAATGATTAC 363
AUTHORS	Homo sapiens		Db	466	AAAGAACACCCAGAATTCCTAGAAGATCATTACACTTCCTCCAGAGATGATCAT 525
TITLE	Bukayrta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		Qy	364	CASACCTGTCCTCGTGTACCCAGGTCGGAAGATTCCTGA 405
JOURNAL	Unpublished (1999)		Db	526	CAGCTCTCTCTCTAGAACACAGGAAGTGAAGATCCTG 567
COMMENT	On Jun 10, 2003 this sequence version replaced gi:31585681.				
ORGANISM	Office of Cancer Genomics				
FEATURES	High quality sequence start: 14				
source	Bldg. 31 Rm10A07 Bethesda, MD 20892				
FEATURES	High quality sequence stop: 600.				
source	Email: cgpb82@mail.nih.gov				
FEATURES	Location/Qualifiers				
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/clone="IMAGE:6971862"					
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/clone_lib="NIH_MGC_195"					
/note="Vector; pDNR-Dual; Site_1: loxP-Sall; Site_2: loxP-HindIII; Clones from this library have been PCR-amplified using gene-specific primers to contain the complete open reading frame (based on known gene sequences available from NCBI's RefSeq). Template for PCR is cDNA derived from either pooled cytoplasmic polyA RNA from 30 cells lines or pooled total RNA from 10 different tissues (from BD Biosciences/Clontech and Washington University). PCR products are directionally cloned into the loxP sites of the pDNR-Dual vector. Library constructed by Dr. Narayan Bhat, Earl Bore III and Hongling Liao (Gene Expression Laboratory, Research Technology Program, SAIC Frederick, NCI-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at <a href="http://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat">http://image.llnl.gov/image/rearrayed_plates/IRBK.preSV.dat</a> a Note: this is a NIH_MGC Library."					
ORIGIN					
Query Match	73.6%; Score 298; DB 5; Length 600;				
Best local Similarity	83.8%; Pred: No. 3.2e-82;				
Matches	337; Conservative 0; Mismatches 65; Indels 0; Gaps 0;				
Qy	4 CAAGCTTCAAGATCCACATGATAGATGCGTCAACTTATAGATATGTTGATCAGTG	63			
Db	166 CAAGCTTCAAGATCCACATGATAGATGCGTCAACTTATAGATATGTTGATCAGTG	225			
Qy	64 AAAATATATGTAATGACCTGTTCCGGATTCCTGGCCGGCTCGGAAGATGTTGAGACC	123			
Db	226 AAAATATATGTAATGACCTGTTCCGGATTCCTGGCCGGCTCGGAAGATGTTGAGACC	285			
Qy	124 ACTGTGACTGTCGCTTTCCTCGTTCAGAAAGCCAGCTGAATCCGAAACACC	83			

Frederick, NCL-Frederick, Frederick, MD 21702). For information on which gene each clone represents, please visit our anonymous ftp site at  
 ftp://image.lnlm.gov/image/rearranged\_plates/1RBK.presv.dat  
 a Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 73.2%; Score 296.4; DB 5; Length 581;  
 Best Local Similarity 83.6%; Pred. No. 1e-81; Mismatches 336; Conservative 0; Indels 0; Gaps 0;  
 Matches 336; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CAGCTCTGAGTCGCCAGATGATGCTCAATTAGATATGATCACCG 63  
 Db 4 CAGGTCAAGATGCCACATGATGATGCTCAATTAGATATGATCACCG 63  
 Qy 64 AAAATTATGATGATGACCTGGTCCGAATTCCTGATGCTCAACTTATAGATATGATGATCACCG 389  
 Db 388 AAAATTATGATGATGACCTGGTCCGAATTCCTGATGCTCAACTTATAGATATGATGATCACCG 329  
 Qy 124 AACTGTTAGTGGTCCGTTCTCTGTTCCAGAAGGCCACGTGAATCGCAACACC 183  
 Db 328 AACTGTTAGTGGTCCGTTCTCTGCTGTTCCAGAAGGCCACGTGAATCGCAACACC 269  
 Qy 184 GGTACAGACGAGCTATCATGAGCTTAAGAACCTAACGTAACCGCTC 243  
 Db 268 GGAACACATGAAAGGATATCATGATCAATTAAAGCTAACGTAACCGCTC 209  
 Qy 244 ACCAACCGCAGCTGTCAGAACACCGCTGACCTGGCCCTCCTGATGTTATGAG 303  
 Db 208 ACAAATCAGGAGGATATCATGATCAATTAAAGCTAACGTAACCGCTC 243  
 Qy 208 ACAAATCAGGAGGATATCATGATCAATTAAAGCTAACGTAACCGCTC 243  
 Db 268 GGAACACATGAAAGGATATCATGATCAATTAAAGCTAACGTAACCGCTC 209  
 Qy 244 ACCAACCGCAGCTGTCAGAACACCGCTGACCTGGCCCTCCTGATGTTATGAG 303  
 Db 304 AAAAACCGCGAAAGAATTCTGGACGCTTCAAATCCCTCTGAGAAATGATGTCAC 363  
 Db 148 AAAAACACCACAAAGGATTCCTAGAAGATTCCTCAAATGATGTCAC 89  
 Qy 364 CAGCACCTGCTCTGATACCACGCTTCCAGAGATTCCTCA 405  
 Db 88 CAGAACTGTCCTCTAGAACACACGGAGTGGATTCCTGA 47

## RESULT 13

AY17615  
 LOCUS AY17615  
 DEFINITION Pan troglodytes IL21 gene, VIRTUAL TRANSCRIPT, partial sequence,  
 ACCESSION AY17615  
 VERSION AY17615.1  
 KEYWORDS GSS,  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 REFERENCE 1 (bases 1 to 489)  
 AUTHORS Clark,A.G., Gianovski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 489)  
 AUTHORS Clark,A.G., Gianovski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
 them based on alignment/Qualifiers  
 FEATURES Location/Qualifiers

## RESULT 14

AY17615  
 LOCUS CR988723  
 DEFINITION CR988723 mRNA sequence.  
 ACCESSION CR988723  
 VERSION 1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 551)  
 AUTHORS Heil,O., Ebert,L., Henning,S., Henze,S., Radelof,U., Schneider,D.,  
 and Korn,B.  
 TITLE Human T-Lymphocytes library  
 JOURNAL Unpublished (2005)  
 COMMENT Contact: Inge Arlart  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Email: www.rzpd.de  
 RZPD: RZPDp016J0144.  
 RZPLIB: (Human T-Lymphocytes), RZPD LIB No. 9016  
 http://www.rzpd.de/cgi-bin/products/set.cgi?libno=9016 Contact:  
 Inge Arlart  
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 100  
 Fax: +49 30 32639 111  
 www.rzpd.de

This clone is available from RZPD;  
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDp9016J0144>  
 contact RZPD (product-support@rzpd.de) for further information.

Primer name: qe3<sup>4</sup>, Primer sequence: CGATTAACATTCACAGC.  
 Location/Qualifiers

FEATURES  
source

1. .551  
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 /clone\_lib="RZPD no. 9016"  
 /note="Vector: pQE80LSN cloned; Site\_1: Sali; Site\_2:  
 NotI; vector: pQE80LSN cloned.pic.shtml  
[http://www.rzpd.de/info/vectors/pQE80LSN\\_cloned.pic.shtml](http://www.rzpd.de/info/vectors/pQE80LSN_cloned.pic.shtml)  
 ; 1st strand cDNA was prepared from mRNA obtained from  
 human T-Lymphocytes with a NotI - oligo(dT) primer [5'  
 GAATGAGCTTACAGTCGGAGCCGCCTTCTTCTTCTT 3'].  
 Double-stranded cDNA was ligated to Sali adaptors,  
 digested with NotI and cloned into the NotI and Sali sites  
 of the pQE80LSN cloned vector"

ORIGIN

Query Match 72.2%; Score 292.6; DB 8; Length 551;  
 Best Local Similarity 82.3%; Pred. No. 1.6e-80;  
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 Qy 4 CAAGGGTCAAGATGCCAACATGATAGAATGGTCAACTTATAGATATTGATCAGCTG 63  
 Db 139 CAAGGGTCAAGATGCCAACATGATAGAATGGTCAACTTATAGATATTGATCAGCTG 198  
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 124 AACTGTGAGTGTGTCGCGCTTCTCCGTGAGAACCTCTGACTCCGGCTCTGATCTATGAG 183  
 259 ACTGTGAGTGTGTCAGTTTCTCGTTCTAGAGGCCAACATTAAGTCAGAACATCA 318  
 184 GTTACACAAACGACGTTCTCAACGGTTCCATAAAATCTGAAACGTTAACGGCGTCC 243  
 319 GAAACAAATGAAAGGATAATCAATGATCAATTAAGCTGAAAGGAAACCTTCC 378  
 244 ACCAACCGGGCTCTGTCAGAACACCTCTGACTCCGGCTCTGATCTATGAG 303  
 379 ACAAATGCGGGAGAACAGAACACATACATGCTCTCATGATCTATGAG 438  
 Qy 304 AAAAACCGGGAAAGAACATTCTGGACCTTCAATCCCTGCTGAGAACATCAC 363  
 Db 439 AAAAACACCCAAAGAACATTCTAGAAAGATCTAAATCTCTCCAAAGATCAT 498  
 Qy 364 CAGGACTCTCTCTGTTACCCACGGTTGCGAACATTCTGAA 405  
 Db 499 CAAATCTGCTCTTAAACACACGGAGTGAATTCCTGA 540

National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 On Jun 10, 2003 this sequence version replaced gi:31585679.  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics

Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgrpb5@mail.nih.gov

Tissue Procurement: Narayan Bhat  
 CDNA Library Preparation: Bhat Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>

Plate: IRBK2 row: 9 column: 07

High quality sequence start: 14  
 Location/Qualifiers

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/tissue\_type="mixed"  
 /lab\_host="DH5A (T1 phage-resistant)"

/clone\_lib="NIH MGC 195"  
 /note="Vector: PDNR-Dual; Site\_1: loxP-Sali; Site\_2:  
 loxP-HindIII; Clones from this library have been

PCR-amplified using gene-specific primers to contain the  
 complete open reading frame (based on known gene sequences  
 available from NCBI's RefSeq). Template for PCR is cDNA  
 derived from either pooled cytoplasmic polyA RNA from 30  
 cells lines or pooled total RNA from 10 different tissues  
 (from BD Biosciences/Clontech and Washington University).  
 PCR products are directionally cloned into the loxP sites  
 of the PDNR-Dual vector. Library constructed by Dr.  
 Narayan Bhat, Earl Bore III and Hongling Liao (Gene  
 Expression Laboratory, Research Technology Program, SAIC  
 Frederick, NCI-Frederick, Frederick, MD 21702). For  
 information on which gene each clone represents, please  
 visit our anonymous PCR site at  
[http://image.llnl.gov/image/rearranged\\_plates/IRBK.presv.dat](http://image.llnl.gov/image/rearranged_plates/IRBK.presv.dat)  
 a Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 69.9%; Score 293.2; DB 5; Length 608;  
 Best Local Similarity 82.7%; Pred. No. 1.5e-77;  
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 Db 166 CAAGGTCAAGATGCCAACATGATATTGAGATGGTCAACTTATAGATATTGATCAGCTG 225  
 Qy 64 AAAATTATGTTGATGACTGTTGCGGATTCCTGGCGCTCGGGAGATGTTGAGCC 123  
 Db 226 AAAATTATGTTGATGACTGTTGCGGATTCCTGGCGCTCGGGAGATGTTGAGAGCA 285  
 Qy 124 AACTGTGAGTGTGTCGCTTCTCTGTTCCAGAAACGCCAGGTGAATTCGCCAACCC 183  
 Db 286 AACGTGTGAGTGTGTCAGTTTCTGTTCTAGAAAGGCCAACATAGTCAGAACATCA 345  
 Qy 184 GGTAACACAGAACCTATATCAAGTTCCATTAAGAACACTGAAACGTAACCGCGCTCC 243  
 Db 346 GAAACACATGAAGGATAATCAATGATCAATTAAGCTGAAAGGAAACCCCTCC 405  
 Qy 244 ACCACGAGGTCTCTGTCAGAACCTCT-----GACTGTGCGCTCTGTT 295  
 Db 406 ACAATGAGGGAGAGAGAACACAGACTATTCTGAGATGCTCTCTGTT 465  
 Qy 296 CTATGAGAAACCGGAGAAATCTGGAACGTTCAATCCCTGCTCAGAGAA 355  
 Db 466 CTATGAGAAACCGGAGAAATCTGGAACGTTCAATCAATCACTCTCCAAAAGA 525

Wed Aug 9 10:48:03 2006

usb-10-735-149-27.rst

Page 11

Qy 356 TGATTCACCAACCGTCCCTCGTACCCAGGTTCCGAAGATTCCCTGA 405  
Db 526 TGATTCATCAGCATCTGCTCTAGAACACCGAAGTGAAGATTCCCTGA 575

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Job time : 4434 secs

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